



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 149976**

**TO: Emily M Le**  
**Location: 3c35/3c18**  
**Art Unit: 1648**  
**Wednesday, April 06, 2005**

**Case Serial Number: 10/674666**

**From: Noble Jarrell**  
**Location: Biotech-Chem Library**  
**Rem 1B71**  
**Phone: 272-2556**

**Noble.jarrell@uspto.gov**

### **Search Notes**

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crfe

149976

**Jarrell, Noble**

**From:** Le, Emily  
**Sent:** Tuesday, April 05, 2005 4:38 PM  
**To:** Jarrell, Noble  
**Subject:** Sequence Search: 10/674666

Noble,

Please provide a search for the following:

1. SEQ ID NO: 1

Thanks!

Emily Le  
Office, Rem 3C35  
Mailbox, Rem 3C18  
Tel., 2-0903

Noble

fr 4/6/05

1 AA; Compugen

5 prep; 5 onl

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:03 ; Search time 1681 Seconds  
(without alignments)  
80.777 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVFDKNGIHVSEIGEL.....LGMNARCMPLSKRDYKW 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	2120	100.0	409	16	US-10-674-666-1
2	2116	99.8	409	16	US-10-674-666-2
3	2112	99.6	409	16	US-10-674-666-3
4	2108	99.4	409	16	US-10-674-666-4
5	1797.5	84.8	409	16	US-10-674-666-7
6	1793.5	84.6	409	16	US-10-674-666-9
7	1793.5	84.6	409	16	US-10-674-666-10
8	1789.5	84.4	409	16	US-10-674-666-8
9	1764.5	83.2	410	16	US-10-674-666-5
10	1763.5	83.2	410	15	US-10-343-175-10
11	1760.5	83.0	410	16	US-10-674-666-6
12	707.5	33.4	410	15	US-10-369-493-16696
13	681.5	32.1	413	16	US-10-674-666-19

14	679	32.0	411	16	US-10-674-666-13	Sequence 13, Appl
15	670.5	31.6	408	16	US-10-674-666-20	Sequence 20, Appl
16	655	30.9	413	16	US-10-674-666-18	Sequence 18, Appl
17	651.5	30.7	409	16	US-10-674-666-14	Sequence 14, Appl
18	651.5	30.7	409	17	US-10-472-928-4502	Sequence 4502, Ap
19	631.5	29.8	410	15	US-10-369-493-18511	Sequence 18511, A
20	625	29.5	409	16	US-10-674-666-21	Sequence 21, Appl
21	612.5	28.9	410	16	US-10-674-666-15	Sequence 15, Appl
22	600.5	28.3	409	16	US-10-674-666-16	Sequence 16, Appl
23	532	25.1	403	15	US-10-369-493-8351	Sequence 8351, Ap
24	519	24.5	406	14	US-10-238-075-715	Sequence 715, App
25	514	24.2	409	15	US-10-156-761-9857	Sequence 9857, Ap
26	486.5	22.9	418	15	US-10-369-493-13732	Sequence 13732, A
27	476	22.5	399	15	US-10-369-493-7149	Sequence 7149, Ap
28	476	22.5	399	15	US-10-369-493-4394	Sequence 4394, Ap
29	467	22.0	401	15	US-10-369-493-4661	Sequence 4661, Ap
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33	154	7.3	81	9	US-09-867-550-164	Sequence 164, App
34	136	6.4	105	15	US-10-424-589-16467	Sequence 16467, App
35	113.5	5.4	1270	14	US-10-032-585-7127	Sequence 7127, Ap
36	113	5.3	743	15	US-10-282-122A-74773	Sequence 74773, A
37	109	5.1	453	15	US-10-282-122A-42589	Sequence 42589, A
38	105	5.0	580	15	US-10-674-666-17	Sequence 17, Appl
39	104.5	4.9	740	15	US-10-282-122A-72237	Sequence 72237, A
40	104.5	4.9	1057	15	US-10-282-122A-70305	Sequence 70305, A
41	104.5	4.9	1057	17	US-10-470-048B-152	Sequence 152, App
42	104	4.9	4688	15	US-10-282-122A-76865	Sequence 76865, A
43	103	4.9	495	17	US-10-282-122A-675-14	Sequence 14, Appl
44	103	4.9	502	15	US-10-282-122A-54571	Sequence 54571, A
45	103	4.9	772	13	US-10-121-032-28	Sequence 28, Appl

#### ALIGNMENTS

RESULT 1  
US-10-674-666-1  
; Sequence 1, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
; FILE REFERENCE: PH08001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominus  
US-10-674-666-1

Query Match 100.0%; Score 2120; DB 16; Length 409;  
Best Local Similarity 100.0%; Pred. No. 3.8e-186;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	61	FKIKDKGINVVELTIDVAETVDASAKAKEEFITETPTEVPVLTANKKAVAFILS	120
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DB	121	KPTHEMVEFMMSGITKVELGVSEENELIVDPMPNLYFRDPPASVGVGVTTHFMRIYR	180

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DB 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVKN 409

RESULT 2
US-10-674-666-2
; Sequence 2, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-2

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Best Local Similarity 99.8%; Pred. No. 8.8e-186;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-674-666-3
; Sequence 3, Application US/10674666
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; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 3
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-3

Query Match 99.6%; Score 2112; DB 16; Length 409;
Best Local Similarity 99.8%; Pred. No. 2e-185;
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 361 IGYDNEKTNALKAAGITVLPFHGNQSLGGMNARCMSMPLSRKDVKN 409

RESULT 4
US-10-674-666-4
; Sequence 4, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 4
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominus
US-10-674-666-4

Query Match 99.4%; Score 2108; DB 16; Length 409;
Best Local Similarity 99.5%; Pred. No. 4.8e-185;
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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## RESULT 5

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US-10-674-666-7
; Sequence 7, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: US 60/427,497
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-7
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Query Match 84.8%; Score 1797.5; DB 16; Length 409;  
Best Local Similarity 84.4%; Pred. No. 1.7e-156;  
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

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Db 61 FVKIMKDRGINVELTDLVAETVYDLASAKAKEEFLETLEETVPVLTANKKAVAFLLS 120
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Db 121 KPTHMEVFPMMSGITKYEIGVSENELIYDPMPNLYFTFDPFASVGNVTIHFMRYYVR 180
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Db 181 RETLFARFVRNHPKLVKTPMYDDPAMKMPLEGSDVFYNNETLVVGSERTDLDITTL 240
QY 240 AKNIKANKVEFEKRIYVAINVPKMTNLMHLDITLMDKNKFLYSPINDVFKFMDYDLV 299
Db 240 AKNIKANKVEFEKRIYVAINVPKMTNLMHLDITLMDKNKFLYSPINDVFKFMDYDLV 300
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Db 361 VIGYDRNEKTNALKAAGITVLPHFGNQLSLGMGNARCMSMPLSRKDYK 409
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## RESULT 6

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US-10-674-666-9
; Sequence 9, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-10-674-666-9
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Query Match 84.6%; Score 1793.5; DB 16; Length 409;  
Best Local Similarity 84.1%; Pred. No. 4.1e-156;  
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

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QY 61 FVKIMKDRGINVELTDLVAETVYDLASAKAKEEFLETLEETVPVLTANKKAVAFLLS 120
Db 61 FVKIMKDRGINVELTDLVAETVYDLASAKAKEEFLETLEETVPVLTANKKAVAFLLS 120
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Db 121 KPTHMEVFPMMSGITKYEIGVSENELIYDPMPNLYFTFDPFASVGNVTIHFMRYYVR 180
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QY 240 AKNIKANKVEFEKRIYVAINVPKMTNLMHLDITLMDKNKFLYSPINDVFKFMDYDLV 299
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## RESULT 7

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US-10-674-666-10
; Sequence 10, Application US/10674666
; Publication No. US20040131604A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
; FILE REFERENCE: PHOE0001-100
; CURRENT APPLICATION NUMBER: US/10/674,666
; PRIOR FILING DATE: 2003-09-29
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PRIOR APPLICATION NUMBER: US 60/427,497  
 PRIOR FILING DATE: 2002-11-18  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: Patent version 3.2  
 SEQ ID NO 10  
 LENGTH: 409  
 TYPE: PRT  
 ORGANISM: Mycoplasma arthritidis  
 US-10-674-666-10

Query Match 84.6%; Score 1793.5; DB 16; Length 409;  
 Best Local Similarity 84.1%; Pred. No. 4.1e-156;  
 Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

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 QY 300 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 408  
 DB 361 VIGYSRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 409

RESULT 8  
 US-10-674-666-8  
 Sequence 8, Application US/10674666  
 Publication No. US20040131604A1  
 GENERAL INFORMATION:  
 APPLICANT: Clark, Mike A.  
 TITLE OF INVENTION: Method for Inhibiting Viral Replication in vivo  
 FILE REFERENCE: PH080001-100  
 CURRENT APPLICATION NUMBER: US/10/674,666  
 PRIOR FILING DATE: 2003-09-29  
 PRIOR APPLICATION NUMBER: US 60/427,497  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: Patent version 3.2  
 SEQ ID NO 8  
 LENGTH: 409  
 TYPE: PRT  
 ORGANISM: Mycoplasma arthritidis  
 US-10-674-666-8

Query Match 84.4%; Score 1789.5; DB 16; Length 409;  
 Best Local Similarity 83.9%; Pred. No. 9.5e-156;  
 Matches 343; Conservative 31; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVSEIGELVTVLHVEPGRIDYITPARLDELFSALIESHDKARKEHQ 60  
 DB 1 MSVDSKFGNGIHVSEIGELSVLVHVEPGRIDYITPARLDELFSALIESHDKARKEHQ 60  
 QY 61 FVKIMKRGINNVVELTDLVAETVYDLASQAKKEFIETFEETVPLTEANKKAVRAFLS 120  
 DB 61 FVALKANDINVEITDVAETVYDLASQAKKRIIEFLDESEPVLSAEKVVRAFLKA 120

DB 61 FVALKANDINVEITDVAETVYDLASQAKKRIIEFLDESEPVLSAEKVVRAFLKA 120  
 QY 121 KPT-HEMVEFMMSGITTYELGVSENELIYDPMNLYFTDPFASVANGVTTHPMRYIVR 179  
 DB 121 KPTSRKLVEMMAGITTYDVGADHDLIYDPMNLYFTDPFASVANGVTTHPMRYIVR 180  
 QY 180 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDITL 239  
 DB 181 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDITL 240  
 QY 240 LAKNITKANKEVEFKRIIVAINVPMKTNLMHLDITWLMIDKKNKFLYSPINDVFKFMDYDLV 299  
 DB 241 LAKNITKANKEVEFKRIIVAINVPMKTNLMHLDITWLMIDKKNKFLYSPINDVFKFMDYDLV 300  
 QY 300 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 408  
 DB 361 VIGYSRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 409

RESULT 9  
 US-10-674-666-5  
 Sequence 5, Application US/10674666  
 Publication No. US20040131604A1  
 GENERAL INFORMATION:  
 APPLICANT: Clark, Mike A.  
 TITLE OF INVENTION: Method for Inhibiting Viral Replication in vivo  
 FILE REFERENCE: PH080001-100  
 CURRENT APPLICATION NUMBER: US/10/674,666  
 PRIOR FILING DATE: 2003-09-29  
 PRIOR APPLICATION NUMBER: US 60/427,497  
 NUMBER OF SEQ ID NOS: 21  
 SOFTWARE: Patent version 3.2  
 SEQ ID NO 5  
 LENGTH: 410  
 TYPE: PRT  
 ORGANISM: Mycoplasma arginini  
 US-10-674-666-5

Query Match 83.2%; Score 1764.5; DB 16; Length 410;  
 Best Local Similarity 82.0%; Pred. No. 1.9e-153;  
 Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVDSKFGNGIHVSEIGELVTVLHVEPGRIDYITPARLDELFSALIESHDKARKEHQ 60  
 DB 1 MSVDSKFGNGIHVSEIGELSVLVHVEPGRIDYITPARLDELFSALIESHDKARKEHQ 60  
 QY 61 FVKIMKRGINNVVELTDLVAETVYDLASQAKKEFIETFEETVPLTEANKKAVRAFLS 120  
 DB 61 FVALKANDINVEITDVAETVYDLASQAKKRIIEFLDESEPVLSAEKVVRAFLKA 120  
 QY 121 KPT-HEMVEFMMSGITTYELGVSENELIYDPMNLYFTDPFASVANGVTTHPMRYIVR 179  
 DB 121 KPTSRKLVEMMAGITTYDVGADHDLIYDPMNLYFTDPFASVANGVTTHPMRYIVR 180  
 QY 180 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDITL 239  
 DB 181 RRETLFARFVFNHPKLVKTPWYDDPAMKPIEGGVFIYNNETLVGVSERTDLDITL 240  
 QY 240 LAKNITKANKEVEFKRIIVAINVPMKTNLMHLDITWLMIDKKNKFLYSPINDVFKFMDYDLV 299  
 DB 241 LAKNITKANKEVEFKRIIVAINVPMKTNLMHLDITWLMIDKKNKFLYSPINDVFKFMDYDLV 300  
 QY 300 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 359  
 DB 301 NGAEPOQNLGFLDKLASIINKEPVLPIGAGATEMEIARETNPDGTNYLAIRKPL 360  
 QY 360 VIGYDRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 409  
 DB 361 VIGYSRNEKTNALKAAGITVLPFHGNOLSLGMGNARCMSPLSRKDYK 409



DB 361 VIGSRNEKTNAALEAAGIKVLPFHGNOQLSLGMGNARCMWPLSRKDYVM 410

RESULT 10  
US-10-343-175-10  
; Sequence 10, Application US/10343175  
; Publication No. US20040096437A1  
; GENERAL INFORMATION:  
; APPLICANT: AngiLab, Inc.  
; TITLE OF INVENTION: The pharmaceutical composition containing arginine deiminase for  
; TITLE OF INVENTION: Inhibiting angiogenesis  
; FILE REFERENCE: PCA/KR01/01281  
; CURRENT APPLICATION NUMBER: US/10/343,175  
; CURRENT FILING DATE: 2003-01-24  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Kopatentin 1.71  
; SEQ ID NO 10  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acids coding Mycoplasma Arginine Deiminase  
US-10-343-175-10

Query Match 83.2%; Score 1763.5; DB 15; Length 410;  
Best Local Similarity 82.0%; Pred. No. 2.4e-153;  
Matches 336; Conservative 37; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVPDSKNGINHYSEIGLETLVHVEPGRIDYITPARLDLPSAIIESHDKREHQS 60  
DB 1 MSVPDSKNGINHYSEIGLESVLVHVEPGRIDYITPARLDLPSAIIESHDKREHQS 60  
QY 61 FYKIMKDCGINVELTDVAETDYDASAKAEEFIEFTPEETVPVLTANKKAVRAFLIS 120  
DB 61 FVAELKANDINVELIDVAETDYDASAKAEEFIEFTPEETVPVLTANKKAVRAFLIS 120  
QY 121 KPT-HEMVEFMMSGITTKYELGVSENELIVDPMNLYFTRDPFASVGNQVTIHFMRYYR 179  
DB 121 KPTSELVEIMMAGITTKYELGVSENELIVDPMNLYFTRDPFASVGNQVTIHFMRYYR 180  
QY 180 RRETFPAPFVFNHKLVTPTWYDPAKMPLEGDVFYNNETLVGVSERTDITL 239  
DB 181 QRETFPAPFVFNHKLVTPTWYDPAKMPLEGDVFYNNETLVGVSERTDITL 240  
QY 240 LAKNIKANKVEFEKRIIVAINVPRKTNLMHLDTWLMDKFLYSPFIANDVFKFMDYDLV 299  
DB 241 LAKSIVANKECEPKRIIVAINVPRKTNLMHLDTWLMDKFLYSPFIANDVFKFMDYDLV 300  
QY 300 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETFDGTNYLAIKPGL 359  
DB 301 NGGAEPOPQNLPLEGLQSIINKKPVLIPIAGGASOMELERETHFDGTNYLAIRPGV 360  
QY 360 VIGSRNEKTNAALEAAGITVLPFHGNOQLSLGMGNARCMWPLSRKDYVM 409  
DB 361 VIGSRNEKTNAALEAAGIKVLPFHGNOQLSLGMGNARCMWPLSRKDYVM 410

RESULT 11  
US-10-674-666-6  
; Sequence 6, Application US/10674666  
; Publication No. US20040131604A1  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: Methods for inhibiting viral replication in vivo  
; FILE REFERENCE: PHE0001-100  
; CURRENT APPLICATION NUMBER: US/10/674,666  
; CURRENT FILING DATE: 2003-09-29  
; PRIOR APPLICATION NUMBER: US 60/427,497  
; PRIOR FILING DATE: 2002-11-18  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 410

; TYPE: PRT  
; ORGANISM: Mycoplasma arginini  
US-10-674-666-6

Query Match 83.0%; Score 1760.5; DB 16; Length 410;  
Best Local Similarity 81.7%; Pred. No. 4.4e-153;  
Matches 335; Conservative 38; Mismatches 36; Indels 1; Gaps 1;

QY 1 MSVPDSKNGINHYSEIGLETLVHVEPGRIDYITPARLDLPSAIIESHDKREHQS 60  
DB 1 MSVPDSKNGINHYSEIGLESVLVHVEPGRIDYITPARLDLPSAIIESHDKREHQS 60  
QY 61 FYKIMKDCGINVELTDVAETDYDASAKAEEFIEFTPEETVPVLTANKKAVRAFLIS 120  
DB 61 FVAELKANDINVELIDVAETDYDASAKAEEFIEFTPEETVPVLTANKKAVRAFLIS 120  
QY 121 KPT-HEMVEFMMSGITTKYELGVSENELIVDPMNLYFTRDPFASVGNQVTIHFMRYYR 179  
DB 121 KPTSELVEIMMAGITTKYELGVSENELIVDPMNLYFTRDPFASVGNQVTIHFMRYYR 180  
QY 180 RRETFPAPFVFNHKLVTPTWYDPAKMPLEGDVFYNNETLVGVSERTDITL 239  
DB 181 QRETFPAPFVFNHKLVTPTWYDPAKMPLEGDVFYNNETLVGVSERTDITL 240  
QY 240 LAKNIKANKVEFEKRIIVAINVPRKTNLMHLDTWLMDKFLYSPFIANDVFKFMDYDLV 299  
DB 241 LAKNIKANKVEFEKRIIVAINVPRKTNLMHLDTWLMDKFLYSPFIANDVFKFMDYDLV 300  
QY 300 NGGAEPOPQNLPLDKLASIINKEPVLIPIGAGATEMEIARETFDGTNYLAIKPGL 359  
DB 301 NGGAEPOPQNLPLEGLQSIINKKPVLIPIAGGASOMELERETHFDGTNYLAIRPGV 360  
QY 360 VIGSRNEKTNAALEAAGITVLPFHGNOQLSLGMGNARCMWPLSRKDYVM 409  
DB 361 VIGSRNEKTNAALEAAGIKVLPFHGNOQLSLGMGNARCMWPLSRKDYVM 410

RESULT 12  
US-10-369-493-16696  
; Sequence 16696, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 16696  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-369-493-16696

Query Match 33.4%; Score 707.5; DB 15; Length 410;  
Best Local Similarity 40.9%; Pred. No. 3.3e-56;  
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVSEIGLETLVHVEPGRIDYITPARLDLPSAIIESHDKREHQSFKIMKDCGI 70  
DB 5 IHVSEIGLETLVHVEPGRIDYITPARLDLPSAIIESHDKREHQSFKIMKDCGI 64  
QY 71 NVELTDVAETDYDASAKAEEFIEFTPEETVPVLTANKKAVRAFLISKTHMVEFM 130  
DB 65 EVLYLEKLAEEA-LVDKRLREEFVDRILKEGQADVVAH-QTLKEYLISFSNEELIQKI 121

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RESULT 13
US-10-674-666-19
? Sequence 19, Application US/10674666
? Publication No. US20040131604A1
? GENERAL INFORMATION:
? APPLICANT: Clark, Mike A.
? TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo
? FILE REFERENCE: PHE00001-100
? CURRENT APPLICATION NUMBER: US/10/674,666
? CURRENT FILING DATE: 2003-09-29
? PRIOR APPLICATION NUMBER: US 60/427,497
? PRIOR FILING DATE: 2002-11-18
? NUMBER OF SEQ ID NOS: 21
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 19
? LENGTH: 413
? TYPE: PRT
? ORGANISM: Bacillus licheniformis
US-10-674-666-19

```

	Query Match	32.1%;	Score 681.5;	DB 16;	Length 413;	
	Best Local Similarity	38.4%;	Fred. No. 8.2e-54;			
	Matches 163;	Conservative 66;	Mismatches 152;	Indels 43;	Gaps 7;	
Qy	11	IHVSEIGLELTVLHVEGRERIDYTPARDLELFSALIESHDARKHOSFYKIMKDRGI	70			
Db	7	IHVSEIGLKVLMKRGRELEMLTEYLERLLFDIPLPRAVQENHQFATLKKQQA	66			
Qy	71	NVVELTDVLAETVYDLASQAKEBRIETFLLEETVPVLTANKKAVRAPIILSKPTHEVEM	130			
Db	67	EVLVLEKTLAEALDGA--LVREQFIIDELLETESKADIGAYDR--LKEFLLTPADSWVEQV	123			
Qy	131	MSGITKVELGVESENEI-----IVPMPLVYTPRPDPAVSNGVTHIMKRYLR	180			
Db	124	MSGIKQLELEBKSHLHELMEDHYPPYLDPMPLVYTPRDAALDSSGLTIINKKEPAR	183			
Qy	181	RETLFARVFNHPCLV--KTPWYTDPAKMPIEGGDVFIYNNETLVGVSERTLDITTT	238			
Db	184	RESLTFMRYIINHPRFKGHEIPVLLDRDFKFNIEGGDEVLNETVAIGVSERTTAQMI	243			
Qy	239	LAAKIKANKKEVPRIVAINVPCWTLMLDLQWLTMDKKNKELYSPIANDVFKWYDL	298			
Db	244	RLVRLD--FQSGRIKRFVLAETIPSGRAFMHLDITFTVMDRDOCTIHPALO-----	292			
Qy	299	VNGAEPOPLNGEPLDLKLASIIINKEPVLIP-----IGGAGATEMEIARE	344			
Db	293	---GPEGDMRIFLVERGKTADIEHTTEBHNLPVLAKRTIGLSVNLIPGGGDELAISARE	349			
Qy	345	TNFDSTNLAIKPGVIGVDPNNEKTNALAKAAGITVLPFHGNQSLGKGNARQMSMPLSR	404			
Db	350	QMNDSNTLAIAPGVVATYDNNYISNECLAEQIKYIEIPSGELSGRGRGPRCSMPLYR	409			

RESULT 14  
US-10-674-666-13  
Sequence 13, Application US/10674666  
Publication No. US20040131604A1  
GENERAL INFORMATION:  
APPLICANT: Clark, Mike A.  
TITLE OF INVENTION: Methods for Inhibiting Viral Replication in vivo  
FILE REFERENCE: PHE0001.100  
CURRENT APPLICATION NUMBER: US/10/674, 666  
CURRENT FILING DATE: 2003-09-29  
PRIORITY APPLICATION NUMBER: US 60/427,497  
PRIORITY FILING DATE: 2002-11-18  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.2

Query Match 32.0%; Score 679; DB 16; Length 411;  
Best Local Similarity 39.4%; Pred. No. 1.4e-53;  
Matches 163; Conservative 70; Mismatches 15; Indels 26; Gaps 10;

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OY 11 HVASEIGLELVVMHBERGRIEDYTPPARIDELLFSALIESHDARKHOSFVKIMDORGI 70
Db 7 HVASEIGLKKVLLHHRGKEIENIMPMYLERILLFDIPLEBDQXCHDAFPAOLRDEGI 66
OY 71 NVVELTDLVAETVYDLSAKAKEEPIETPLEETVULTEANKKAVRALLS-KPHHEVVEF 129
Db 67 EULVJETTLAABS--LVTPETREAFIDETLS-ANIRGATKKAIRELIMAEIDNOETIEK 123
OY 130 MMSGTTYELG-----YESENEI,VDMPNLYTPRODPFASVGNGVTIHFERYI 177
Db 124 TWAGVQXSELPEIPASEKGLTDLVESNVPRAIDPMPLVFTLRDPFALIGVGSILMHFSE 183
OY 178 VPRRETLFARFVFRNHPTL--VKTPWYTDPMKMPREGDVFYNNETLVGVGSERTDLD 235
Db 184 TENRETLTGKXIPTHHPYGGGKVPMYDYDRNETTRIGGDELVYSKVLAVGISORTDAA 243
OY 236 TITTLAKKIKANKEVEFGRIVAIIVPKWTIMHLDPTMLDKXKPLYSB-IANDVPKEM 294
Db 244 SIEKLLVNI-FKONIGFPKVLAFEPANNRKPMLHDYFTVWDYDKFTIHEIGEDLRV-- 300
OY 295 DYDLVNGGABOPOLNGLPLDKLLASIIINKRPV-LPIPGAGATEMEIAETPFDGNTYL 353
Db 301 -YSVTVYDNEELHIVEEKDILAEILLAMILGVKVDLJINGGDNL--VVAAGREQNDGNSNTLL 357
OY 354 AIKBPVLGYBRNEKTNALKAAGITVLPFHYGNOLSLGMNAPOMSPISRKOV 407
Db 358 TIABPVVVVVNRNTITNAIESKELIKIJHSELVYGRGGPOMSPFERREI 411

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1  RESULT 15
2  US-10-674-666-20
3  / Sequence 20, Application US/10674666
4  / Publication No. US20040131604A1
5  / GENERAL INFORMATION:
6  / APPLICANT: Clark, Mike A.
7  / TITLE OR INVENTION: Methods for Inhibiting Viral Replication in vivo
8  / FILE REFERENCE: PHE0001-100
9  / CURRENT APPLICATION NUMBER: US/10/674,666
10 / CURRENT FILING DATE: 2003-09-29
11 / PRIOR APPLICATION NUMBER: US 60/427,497
12 / PRIOR FILING DATE: 2002-11-18
13 / NUMBER OF SEQ ID NOS: 21
14 / SOFTWARE: PatentIn version 3.2
15 / SEQ ID NO 20

```

LENGTH: 408  
TYPE: PRF  
ORGANISM: Enterococcus faecalis  
US-10-674-666-20

Query Match 31.6%; Score 670.5; DB 16; Length 408;  
Best Local Similarity 37.9%; Pred. No. 8.3e-53;

Matches 156; Conservative 87; Mismatches 146; Indels 23; Gaps 10;

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QY 11 IHVYSEIGLELVVHPEGRIDYITPALDELLESAIISHDARKEHOSFYKIMKRG1 70
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 5 INVFSIEIGLKTVMLEHPPGKELENLMPDYLERLLFDIPLEKACQAEHDAFAELLRSKD1 64
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 71 NVVELTDLVAETVYDLASKAKAEFEFTPEETVPVLTANKKAVRAFLLS-KPTHEMVEP 129
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 65 EYVYLEDLAELA-LINEEVRRQFIDQFLSE-ANIRSESACEKVRLEMLLEIDNNEELIQK 121
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 130 NMSGITKVELG-----VESENELIVDPMPNLFTTRDPFASVNGVTHFMRYIVR 179
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 122 ATAGIQKQELPKVEQEFLLDMVEADVPFIIDPMPNLFTTRDPFATMGHISLNHMYSVTR 181
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 180 RRETLFARFVFRNHPKLV-KTPWYDPMKMPISGQVFIYNNETLVVGVSEKIDDTI 237
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 182 QRETIFGQYIFDYHPRFAGKEVPRVDRSESTRIEGDELILSKEVVAIGISQRTDAASI 241
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 238 TLLAKNIKANKKEVEPRIVAINVPMKWTNLMHLDTWLDMKKKELVSP-IANDVFKEMDY 296
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 242 EKIAKNITFEQK-LGFKNITLAFDIGHRKFMHLDVFTMTDYDKFTIHPEIBGGLVVSIT 300
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 297 DLVNGGAEPQOLNGLPLDKLASIINKEPV-LIPIGAGATEMEIARETNFDGTYLAI 355
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 301 EKADGDIDQITKED--TLDNITLCKYHLNVLIRGAGNLT-AAAREQWMDGSNTLAI 356
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 356 KEGLVIGYDRNEKTNAAKAGITVLPHGNQSLGNGNARCMSMPLSRKV 407
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 357 APGEVVVYDRNFTITNKALEAGVKNLYIPGSELVGRGGRCSMPLVREDL 408
   ||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
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Search completed: April 6, 2005, 06:23:14  
Job time : 1683 secs

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Db 61 FVAELKANDINVELIDVASTYDLASQAKDKLIBEFLESEPVLSSEHKVVVNFKA 120

Qy 121 KPT-HEMVFMVMSGITKVELGVSENELIVDPMPNLVFTTRDPFASVGVNGVTIHFMRVIVR 179

Db 121 KKTSRKLVIEIMAGITKYDLGLEADHELIVDPMPNLVFTTRDPFASVGVNGVTIHFMRVIVR 180

Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPIDEGDVFIYNNETLVGVVSERTDITL 239

Db 181 QRETLFSRFFVSNHPKLVINTPMYDPSIKLSIEGGDVFIYNNETLVGVVSERTDITL 240

Qy 240 LAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANVDFKFWYDYL 299

Db 241 LAKNIVANKECFKRIIVAINVPKWTNLMHLDITLMDKNKFLYSPIANVDFKFWYDYL 300

Qy 300 NGGAEPQPOLNGLPDLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTYLAIKPGL 359

Db 301 NGGAEPQPVENGLPLEGLLSQIINKPVLPIPIAGSASQMEIERETHFDGTYLAIRPGV 360

Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMNARCMSPLSRKDV 409

Db 361 VIGYSRNEKTNAAEAGIKVLPFHGNQSLGGMNARCMSPLSRKDV 410

RESULT 2

S68515

probable arginine deiminase (EC 3.5.3.6) - Mycoplasma arginini (fragment)

C:Species: Mycoplasma arginini

C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 07-Dec-1999

C:Accession: S68515; S68514

R:Wilm, M.; Shevchenko, A.; Houthaeve, T.; Breit, S.; Schweigerer, L.; Fotsis, T.; Mann, Nature 379, 466-469, 1996

A:Title: Femtomole sequencing of proteins from polyacrylamide gels by nano-electrospray

A:Reference number: S68514; MUID:96158883; PMID:8559255

A:Status: nucleic acid sequence not shown

A:Accession: S68515

A:Molecule type: DNA

A:Residues: 1-410 <WIL>

A:Cross-references: EMBL:X93471

A>Note: only a part of the translation is shown

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995

A:Accession: S68514

A:Molecule type: protein

A:Residues: 103-105,'X',107-111;126,'XX',129-134,'X',136-137;161-167,'D',169-171,'X',173

A:Note: peptides obtained by mass spectrometry

C:Genetics:

C:Genetic code: SGC3

C:Superfamily: arginine deiminase arca

C:Keywords: hydrolase

Query Match 80.3%; Score 1702.5; DB 2; Length 410;

Best Local Similarity 78.3%; Pred. No. 4.6e-113;

Matches 321; Conservative 48; Mismatches 40; Indels 1; Gaps 1;

Qy 1 MSVFSKFNIGHYISEIGLETVLVHPEGRIDYITPARDELLEFSAILEDHARKEHOS 60

Db 1 MSVFSKFNIGHYISEIGLETVLVHPEGRIDYITPARDELLEFSAILEDHARKEHOS 60

Qy 61 FVKIMKDRGINVELDITVAETDLSKAAKEFIETLEETVPLTEANKKAVRAFLLS 120

Db 61 FVEILKQGINVELDITVAETDLSKAAKEFIETLEETVPLTEANKKAVRAFLLS 120

Qy 121 -KPTHEMVFMMSGITKVELGVSENELIVDPMPNLVFTTRDPFASVGVNGVTIHFMRVIVR 179

Db 121 LKSTKELIYNMAGITKYDLGLEADHELIVDPMPNLVFTTRDPFASVGVNGVTIHFMRVIVR 180

Qy 180 RRETLFARFVRNHPKLVKTPWYDPAKMPIDEGDVFIYNNETLVGVVSERTDITL 239

Db 181 QRETLFSKFIETNHPKLVKTPWYDPAKMPIDEGDVFIYNNETLVGVVSERTDITL 240

Qy 240 LAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANVDFKFWYDYL 299

Db 241 LAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSPIANVDFKFWYDYL 300

Qy 300 NGGAEPQPOLNGLPDLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTYLAIKPGL 359

Db 301 NGGSNPEPVVNGLPDLKLLSIIINKKPVLPPIAGKATIEPAVETHFDGTYLAIKPGV 360

Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMNARCMSPLSRKDV 409

Db 361 VIGYSRNVKTNAALEANGIKVLPFGNQLSLGMIARCMSPLSRKDV 410

RESULT 3

A38835

streptococcal antitumor protein - Streptococcus pyogenes

C:Species: Streptococcus pyogenes

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C:Accession: A38835; A33225; S16694

R:Kanaoka, M.; Kawanaka, C.; Negoro, T.; Fukita, Y.; Taya, K.; Agui, H. Agric. Biol. Chem. 51, 2641-2648, 1987

A:Title: Cloning and expression of the antitumor glycoprotein gene of Streptococcus pyogenes

A:Reference number: JE0061

A:Accession: A38835

A:Molecule type: DNA

A:Residues: 1-411 <KAN>

A:Cross-references: UNIPROT:P16962; EMBL:X55659; NID:947340; PIDN:CAA39192.1; PID:947341

R:Kanaoka, M.; Negoro, T.; Kawanaka, C.; Agui, H.; Nabeshima, S. Agric. Biol. Chem. 55, 743-750, 1991

A:Title: Streptococcal antitumor protein: expression in Escherichia coli cells and proper

A:Reference number: JH0364; MUID:91234346; PMID:11368629

A:Accession: A33225

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-57 <KA2>

C:Superfamily: arginine deiminase arca

Query Match 32.0%; Score 679; DB 2; Length 411;

Best Local Similarity 39.4%; Pred. No. 1.5e-40;

Matches 163; Conservative 70; Mismatches 155; Indels 26; Gaps 10;

Qy 11 IHVYSEIGLETVLVHPEGRIDYITPARDELLEFSAILEDHARKEHOSFVKIMKDRGI 70

Db 7 IHVYSEIGLKKVLLHHPFGKEIENLMPDYLERLLFDDIPFLEDAQKEDHAFQAALRDEGI 66

Qy 71 NVVELTDLVAETDLSKAAKEFIETLEETVPLTEANKKAVRAFLLS-KPTHEMVFM 129

Db 67 EVLYLETLAAS--LVTPREAFIDYLS--ANIRGATKKAIRELLMALEDNQELIEK 123

Qy 130 MMSGITKVELG-----YESNELIVDPMPNLVFTTRDPFASVGVNGVTIHFMRVY 177

Db 124 TMAGVQKSELPEIPASEKGLTDLVESVYPAIDPMPNLVFTTRDPFATIGTGVSLNMFSE 183

Qy 178 VRRRETLFARFVRNHPKLV--VKTPWYDPAKMPIDEGDVFIYNNETLVGVVSERTDLD 235

Db 184 TRNRETLGKYIFTHHPYGGKVPWYDRNETTRIEGGDELVLKQDLAVGISQRTDAA 243

Qy 236 TITLAKNIKANKVEFKRIVAINVPKWTNLMHLDITLMDKNKFLYSP-IANDVFKFW 294

Db 244 SIEKLLVNI-FKQNLGFKKVLAFEPANRRKFWLDTVFTWVDYDKFTIHEIGDLRV-- 300

Qy 295 DYDLVNGGAEPPQQLNGLPDLKLLASIIINKEPV-LIPIGGAGATEMEIARETNFDGTYL 353

Db 301 -YSVTYDNEELHIVEEGDLAELLAANLGVKVDLIIRCGDNL--VAAGREQWMDGSNTL 357

Qy 354 AIKPGVLVIGYDRNEKTNAAKAAAGITVLPFHGNQSLGGMNARCMSPLSRKDV 407

Db 358 TIAPGVVVVYRNTITNAILSKGLKLIKHSSELVGRGPRGRCMSMPFEREDI 411

RESULT 4

D95251

arginine deiminase [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 09-Jul-2004

C:Accession: D95251

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

```

177 IYRRETLFARVFRNHPKL--VKTPWYDPAKMPIEGDFIYNNETLWCVGVSERTDL 234
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

Db 177 PARRRESFIELILKHHPFSSQEIPIWSGREBPFPFEGGDELIILNEETVLVGVSERTDA 236  
Qy 235 DTITLLAKNIKANKVEFKRIIVAINVPKWTNLMHLDTWLTMLDKMKELYSP-IANDVFKF 293  
Db 237 RAVELAESL-FSRAPKIKRVLAASIPETRSMHLDTVFTWVNFQAFTIHPAIQOQOGL 295  
Qy 294 WYDYL--VNGGAPQOLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMEIARETNFDGT 350  
Db 296 NVVILEKSENGLEITPRD---FKRVIAEVLGVPEVDIFPCGGEDV--IVSAREQWNGDA 350  
Qy 351 NYLAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
Db 351 NTLAIAPGEVITYDRNHVSNLLRRKAGIKVHEVISSELSRGRGPRCMTMPITRGNLK 408  
RESULT 7  
AD1080  
arginine deiminase homolog lmo0043 [imported] - Listeria monocytogenes (strain EGD-e)  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD1080  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Kars, U.  
Science 294, 849-852, 2001  
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,  
A:Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1080  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-410 <GLA>  
A:Cross-references: UNIPROT:O8VAS0; GB:NC\_003210; PIDN:CAC98258.1; PID:gl6409402; GSPDB:  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo0043  
C:Superfamily: arginine deiminase arca  
Query Match 29.8%; Score 632; DB 2; Length 410;  
Best Local Similarity 37.5%; Pred. No. 3.2e-37;  
Matches 156; Conservative 78; Mismatches 152; Indels 30; Gaps 11;  
Qy 11 IHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKORGI 70  
Db 7 LNIITSEIGKQTLVKRPGSELENTTPEYLSLLFDDIPYLKMWQKEHDFFAKTWRDSNI 66  
Qy 71 NVVELTDLVAETYDLASAKAEFEFTETFEETVLPVLTANKKA--VRAFLLSKPTHEKVE 128  
Db 67 EVLYLEKLAALREANN--KESFLTMIKES---NQMBESALYVRDYLMSFDEEEMIR 120  
Qy 129 FMSGITKYELGVSENEL-----IVDPENLYFTDRPPASVGVNGVTIHFMYIV 178  
Db 121 KMGLKKESEIPERKKGHLNEMDQYFFLDPLFNLYFTDRPAVINGVGTINRMFQPA 180  
Qy 179 RRRETLFARFVRNHPKLVK--TPWYDPAKMPFEGGDVFIYNNETLVVGVSERTDIDT 236  
Db 181 RRRESIFTELILKHHPSPNQDIPWSGRGPFPFSLGGDELVLEETVLVGVSERTDARA 240  
Qy 237 ITLLAKNIKANKVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDVFKFWD 295  
Db 241 VERLAESL-FNRSPIKIKVLAIVEIPETRSMHLDTVFTWVNFQAFTIHPAIQOQOGLNI 299  
Qy 296 YDL--VNGGAPQOLNGLPLDKLLASIIINKEPV-LIPIGGAGATEMEIARETNFDGTNY 352  
Db 300 YILEKSENGLEITPRD---FORVIAEVLDPEDIFPCGGEDV--IVSAREQWNGDANT 354  
Qy 353 LAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
Db 355 LAIAPGEVITYDRNQVSNLLRSAGIKVHEVISSELSRGRGPRCMTMPVLVRENLK 410  
RESULT 8

E86879  
arginine deiminase (EC 3.5.3.6) [imported] - Lactococcus lactis subsp. lactis (strain IL)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: E86879  
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: E86879  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-410 <STO>  
A:Cross-references: UNIPROT:P58013; GB:AB005176; PID:gl2725086; PIDN:AAK06135.1; GSPDB:G  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arca  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase  
Query Match 29.8%; Score 631.5; DB 2; Length 410;  
Best Local Similarity 37.3%; Pred. No. 3.4e-37;  
Matches 156; Conservative 70; Mismatches 163; Indels 29; Gaps 6;  
Qy 9 NGIHVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDR 68  
Db 3 NGINVNSEIGKLSVLLHRPGAEVENITPDMKQLLFDIPYLKIAQKEHDFFAQTLRDN 62  
Qy 69 GINVELTDLVAETYDLASAKAEFEFTETFEETVLPVLTANKKAVRAFLLSK 121  
Db 63 GAETVYIENLATEVFEKSS--TKEEFLSHLLHEAGYRPGRTYDGLTE-----YLTSM 113  
Qy 122 PTHMEVFMMSGITKYEL-----GVESNELIVDPMPLXYETROPFASVGVNGVT 170  
Db 114 STKMVEKIYAGVRKNELDIKRTALSMDAGSDAENYFNLNPLFNAYFTRPOQASGVGMT 173  
Qy 171 IHFMRYIVRRRETLFARFVRNHPKLVKTPWYDPAKMPFEGGDVFIYNNETLVVGVSE 230  
Db 174 INKWTPPARQPESLITEYVMANHPFKDTPWRDRNHTTRIEGGDELILNKTTVVIGVSE 233  
Qy 231 RTDLDTITLLAKNIKANKVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKFLYSP-IANDV 290  
Db 234 RTSKTIQNLAKELFANPLSTFDTVLAVEIPHNNHAMHLDTVFTMINHDQFTVPFGIMDG 293  
Qy 291 FKFWDYDLVNGGAPQOLNGL-PLDKLLASIIINKEPVLPVIGGAGATEMEIARETNFDG 349  
Db 294 AGNINVILRPGKDDVEIEHLTDLKAALKVIMSELIDLIECAG-DPIAAPREQWNDG 352  
Qy 350 TNYLAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407  
Db 353 SNTLAIAPGEIVTYDRNVYTVVELLKEHGKIKVHEITLSELGRGRGCMSQPLWREDL 410  
RESULT 9  
T46741  
arginine deiminase (EC 3.5.3.6) [validated] - Lactobacillus sakei  
C:Species: Lactobacillus sakei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T46741  
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C  
J. Bacteriol. 180, 4154-4159, 1998  
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of t  
A:Reference number: 223141; MUID:98361904; PMID:9696763  
A:Accession: T46741  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-409 <ZUN>  
A:Cross-references: UNIPROT:O53088; EMBL:AJ001330; NID:g2764610; PIDN:CAA04682.1; PID:g2:  
C:Genetics:  
A:Gene: arca  
C:Function:  
A:Description: EC 3.5.3.6 [validated, MUID:98361904]  
A:Pathway: arginine catabolism



C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 29.5%; Score 625; DB 2; Length 409;  
Best Local Similarity 37.4%; Pred. No. 9.8e-37;  
Matches 153; Conservative 77; Mismatches 159; Indels 20; Gaps 8;

```
QY 11 IHVSEIGELEVTVLHVEHGREIDYITPARLDELLFSAILESADARKEHOSFVKIMKDRGI 70
DB 5 IHVSEIGKGLTVLLKRPKEVENITPDIMYRLFFDDIPYLPYIQKEHDDQFAQTLRDNGV 64
QY 71 NVVELTDLVAETDYLASKAAKEEFTETLEETVPVLTANKKAVRAFLLSKPTHEMVEFM 130
DB 65 EVLYLENLAEAIDAGD--VKBAFLDKMLNES-HIKSQVQAALXDYLISWATLDMVEKI 121
QY 131 MSGITKYLGVES-----ENELVDPMNLYFTRDPPASVGVNGVTIHFMYIYVRR 180
DB 122 MAGVRTNEIDIKSKALIDVADDDYFPYMDPMPNLYFTRDPAASMGDLTKINTMFEARQ 181
QY 181 RETLFARFVRNHPKLVK--TPWYYDDPAMKPIEGDVFYINNETLVGVSBERTDLDTIT 238
DB 182 RESMFEVIMQHPRFANQGAQVWRDRDHIDRMGGDELILSDKVLAIQISORTSAQSIE 241
QY 239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMDKNKFLYSPANDVFKFWD-YD 297
DB 242 ELAKVLFPNHS-GFEKILAIKIPHKAMMHLDTVFTMIDYDKFTTHPGIQGAGGMVDYIY 300
QY 298 LVNGGAEPQQLNGPLDKLASIIN-KEPVLIPIGGAGATEMEIARETNFDTGNTYLAIK 356
DB 301 LEPGNNDKIKITHQTDLEKVLRLDALEVPETLIPCGGDA--VVAPEQWNGDSNTLAIA 358
QY 357 POLVIGYDRNEKTNAAKAGITVLPFGNQLSLGNGNARCMSPLSRK 405
DB 359 PGVVVYDRNYVSNENLRQYGIKIVTEVPSSLSRGGPRCMSGMLPLVR 407
```

## RESULT 10

H70204  
arginine deiminase (arca) homolog - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: H70204  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kurlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943; PMID:9403685  
A:Accession: H70204  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-410 <KLE>  
A:Cross-references: UNIPROT:O51781; GB:AE001183; GB:AE000783; NID:G2688786; PIDN:AAC6719  
A:Experimental source: strain B31  
C:Superfamily: arginine deiminase arca

Query Match 28.9%; Score 612.5; DB 2; Length 410;  
Best Local Similarity 36.5%; Pred. No. 7.6e-36;  
Matches 152; Conservative 73; Mismatches 161; Indels 31; Gaps 10;

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QY 9 NGIHVYSIGELEVTVLHVEHGREIDYITPARLDELLFSAILESADARKEHOSFVKIMKDR 68
DB 7 NPINIFSEIGRLKVLHRRPGELENLPLIMKNFLFDDIPYLVKVARQEHEVFNILKDN 66
QY 69 GINVELDLVAETDYLASKAA-KEEFTETLEEVTVLTPANKKAVRAFLLSKPTHEMV 127
DB 67 SVEIEYVEDLVSEV--LASSVALKNKFIQSFILE-AEIKTDGVINILDKYFSNLFTVDNMV 123
QY 128 EFMMSGITKYEL-----GVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIYV 178
DB 124 SKMISGVAREELKCOCEFSLDDWNGSSLFVDPMPNLYFTRDPPASVGVNGVTIHFMYIYV 183
```

```
QY 179 RRRETLFARFVRNHPKLVK-TPWYYDDPAMKPIEGDVFYINNETLVGVSBERTDLDTI 237
DB 184 RRRETIFAEYIFKYHAYKENVPPIWFNRSWEETSLEGGDFVFLNKDLLLVIGISRTAEGSV 243
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMDKNKFLYSPANDVFKFWDYD 297
DB 244 EKLAASLFPNK-APFSTILAFKIPGRAYMHLDTVFTQIDYS--VFTSFTSDDMYFSIYV 300
QY 298 LVNGGAEPQQLNGPLDKLASIINKEPVLPIPTGG-----AGATEMEIARETNFDTG 350
DB 301 LTYNS-----NSNKINIKKEKAKL--KDVLSFYLRKIDIIKACGGDLIHGAREQWNDGA 353
QY 351 NYLAIKPGLVIGYDRNEKTNAAKAGITVLPFGNQLSLGNGNARCMSPLSRKDV 407
DB 354 NVLAIAPEGEVIAYSRNVHTNKLFBENGIKVHRIPSSLSRGGPRCMSGMLSLVRDI 410
```

## RESULT 11

S73857  
arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein H10\_orf198  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73857  
R:Himmelreich, R.; Hilbert, H.; Plegens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73857  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-198 <HIM>  
A:Cross-references: EMBL:AE000052; GB:U00089; NID:G1674223; PIDN:AAB96179.1; PID:G167422;  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: arca  
A:Genetic code: SGC3  
C:Keywords: hydrolase

Query Match 25.5%; Score 540; DB 2; Length 198;  
Best Local Similarity 55.3%; Pred. No. 3.8e-31;  
Matches 109; Conservative 30; Mismatches 52; Indels 6; Gaps 2;

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QY 211 IEGDVFYINNETLVGVSBERTDLDTITLLAKNIKANKEVEFKRIVAINVPKWTNLMHLD 270
DB 4 IEGDIFVYDQQTVMGLSERTTEAAINVLAKKIQDSSTSFKRIVINPQLPNLMHLD 63
QY 271 TWLTMDKNKFLYSPANDVFKFWDYDLVNGAEPQPOLNGL--PLDKLLASIIINKEPVL 328
DB 64 TWLTMDKNKFLYSPNMLAVLKAWRIDF---TDPALKWNEIAGDLSTILHTIIGOKPML 119
QY 329 IPIGGAGATEMEIARETNFDTGNTYLAIKPGLVIGYDRNEKTNAAKAGITVLPFGHQL 388
DB 120 IPIAGADANQVEIDIEHFDGNTYLTAPSVVGYARNKLTHTLEAAGVKVIAFKGNQL 179
QY 389 SLGNGNARCMSPLSRK 405
DB 180 SLGNGSARCMSPVLRK 196
```

## RESULT 12

AB1060  
arginine deiminase (EC 3.5.3.6) [imported] - Salmonella enterica subsp. enterica serovar  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C:Accession: AB1060  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; MUID:21534947; PMID:11677608  
A:Accession: AB1060  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-406 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD06927.1; PID:g16505575; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY4805  
C:Superfamily: arginine deiminase arca  
C:Keywords: hydrolase

Query Match 25.0%; Score 531; DB 2; Length 406;  
Best Local Similarity 32.9%; Pred. No. 4.4e-30;  
Matches 136; Conservative 74; Mismatches 172; Indels 32; Gaps 9;

QY 13 VYSEIGELTVLVHPEGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDRGINV 72  
DB 6 VQSEIGQLRSVMHRPNLSKRLTFNSCQELFFDDVLSVERAGEHDIFANTLRQGGIEV 65  
QY 73 VELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMFMS 132  
DB 66 LLTDLTLTQTLVDAD--AKAWLLDTQISDY--RLGPTTAAADIRAWLADMPHRELARHLSG 121  
QY 133 GITKVELGVSEB-----NELIVDPMPNLVYFRDPPFASVGVNGVTTHFMRYIVRRRET 183  
DB 122 GLTYGEIPASIKNMVVVDTHINDFMKPLNHLFTRDTSCWYINGVSINPMAPARQRET 181  
QY 184 LPARVFNHRHPKLVKTPWY-----YDPAMKMPIEGGDVFIYNNETLVVGVSEDTL 234  
DB 182 NNLRARIYRWHPOFADGDFIKYGDENINYDHA---TLGGDVLVIGRAVLIGMSERTTP 238  
QY 235 DTITLLAKNIKANKKEVEFKRIVAINVPKWTNLMHLDTWMLDKNKF-LYSPINDVFKF 293  
DB 239 QGVFLAQLFKHQAE--RVIAVELPKHRSCHWLDVTWTHIDITDFSYPEVVRPDVQC 296  
QY 294 WDYDLVNGAEPQPLNGPLDKLLASINKEPVLIPGGAGATEMEIARETNGTNYL 353  
DB 297 W--TLTPDGRGLKRTQBSTLVALETALGIDQVRLITTTGGDAFEAE--REQWNDANNVL 352  
QY 354 AIKPLGLVIGYDRNEKTNAAKAAAGITVLPFGNQLSLGMGNARCMSPLSRKDV 407  
DB 353 TLRPQVVGVYERNIWTNEKYDAGITVLPFGDELGRGGRGARCMSCLPDRDGI 406

RESULT 13  
F82323  
arginine deiminase VC0423 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: F82323  
R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, H  
1. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: AB2035; MUID:20406833; PMID:10952301  
A:Accession: F82323  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-407 <HEI>  
A:Cross-references: UNIPROT:O9KUU2; GB:AE004130; GB:AE003852; NID:g9654845; PIDN:AAF9359  
A:Experimental source: serogroup O1; strain N16961; biotype E1 Tor  
C:Genetics:  
A:Gene: VC0423  
A:Map position: 1  
C:Superfamily: arginine deiminase arca

Query Match 23.7%; Score 502.5; DB 2; Length 407;  
Best Local Similarity 31.8%; Pred. No. 4.7e-28;  
Matches 134; Conservative 79; Mismatches 171; Indels 37; Gaps 9;

QY 9 NGIHVYSIGELETVLVHPEGREIDYITPARLDELFSAILSHDARKEHQSFVKIMKDR 68

DB 2 NRLVGVSEVGQLRRVLLNRPERALTHLTTPSNCHELLFDDVLAVEAAGVEHDAFANTLRQ 61  
QY 69 GINVELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAFLLSKPTHEMVE 128  
DB 62 DVEVILLHDLLEET--LAIPAROWLLNTQISDRFGPTFA--RELRLHMLNHLDDHLLTT 117  
QY 129 FMMSGITKVELGVSEB-----ELIVDPMPNLVYFRDPPFASVGVNGVTTHFMRYIVR 179  
DB 118 LLGLGLAFSELHLESDSMLPKMRQPLDFVIEPLNHLFTRDTSCWYGVGSINPMKPAR 177  
QY 180 RRETLPARFVFNHRHPKLVKTPW-----YDPAMKMPIEGGDVFIYNNETLVVGVSE 230  
DB 178 QRETNHLRAIYRWHPIFAQHPIHYFGIDDLHYDNA---NIEGGDVLVIGKGAVLIGMSE 234  
QY 231 RTDLDTTLTLAKNIKANKKEVEFKRIVAINVPKWTNLMHLDTWMLDKNKFELYSPIANDV 290  
DB 235 RTSQGVENLAAL--FKHQASKVIAINLPKRSCHWLDVTWTHMDVDTFSVTP--EV 289  
QY 291 PKFDYDYLNGAEPQPLNGPLDKLLASINKEPVL-----IPGGAGATEMEIARETN 346  
DB 290 MR---KDLPTWRLTPKNGGDMRVEQVPSYLAHQALGVLDYKLIITTGGNSYEAREQW 346  
QY 347 PDGTYLAIKPLGLVIGYDRNEKTNAAKAAAGITVLPFGNQLSLGMGNARCMSPLSRKD 406  
DB 347 NDANNVLTVKPGVVIGYERNVYTNKEYDKAGIKVLTIPGDELGRGGRGARCMSCLPDRDG 406  
QY 407 V 407  
DB 407 I 407

RESULT 14  
S73858  
arginine deiminase (EC 3.5.3.6) arca - Mycoplasma pneumoniae (strain ATCC 29342)  
N:Alternate names: hypothetical protein H10\_Orf238  
C:Species: Mycoplasma pneumoniae  
A:Variety: ATCC 29342  
C>Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 07-Dec-1999  
C:Accession: S73858  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A>Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73858  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-238 <HIM>  
A:Cross-references: EMBL:AE000052; GB:U00089; NID:g1674223; PIDN:AAB96180.1; PID:g167422f  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: arca  
A:Genetic code: SGC3  
C:Keywords: hydrolase

Query Match 23.1%; Score 490; DB 2; Length 238;  
Best Local Similarity 50.3%; Pred. No. 1.7e-27;  
Matches 97; Conservative 43; Mismatches 47; Indels 6; Gaps 3;

QY 7 KFGIHVYSIGELETVLVHPEGREIDYITPARLDELFSAILSHDARKEHQSFVKIMK 66  
DB 2 KYN-INHVSEIGLQTVLVHPTGNEIRNRISPRLLDILLFSAVIEPDTAIOEHQTFCOLLQ 60  
QY 67 DRGINVVELTDLVAETDYLASKAAKEEFITFLEETVPVLTEANKKAVRAFL--SKPT 123  
DB 61 EQNIEVVQLTDLTATTFDKANATAQNFIEQLDQAEPKLTPEHRKAKQVLEQAKST 120  
QY 124 HEMVEFMMSGITKVELGVSEB--ENELIVDPMPNLVYFRDPPFASVGVNGVTTHFMRYIVRRR 181  
DB 121 LSWVRSMGMDIKRKAANAANTINGDFLVDMPNLVYFRDPPFASIGHGHSINRMKYLTRR 180  
QY 182 ETLPARFVFNHRHP 194  
|||||

Job time : 21 secs

Db	181	ETLFASFILPTTP	193
RESULT 15			
C95376			
probable arginine deiminase (EC 3.5.3.6) [imported] - Sinorhizobium meliloti (strain 102			
C/Species: Sinorhizobium meliloti			
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004			
C/Accession: C95376			
R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowe			
: Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.			
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001			
A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti			
A/Reference number: A95262; MUID:21396509; PMID:11481432			
A/Accession: C95376			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-419 <KUR>			
A/Cross-references: UNIPROT:Q92YG5; GB:AE006469; PIDN:AAK65573.1; PID:gl4524052; GSPDB:G			
A/Experimental source: strain 1021, megaplasmid pSymA			
R/Gallibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,			
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;			
L.; Hyman, R.W.; Jones, T.			
Science 293, 668-672, 2001			
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,			
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.			
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.			
A/Reference number: A96039; MUID:21368234; PMID:11474104			
A/Contents: annotation			
C/Genetics:			
A/Gene: arcA2			
A/Genome: plasmid			
C/Superfamily: arginine deiminase arca			
C/Keywords: hydrolase			
Query Match 22.8%; Score 484; DB 2; Length 419;			
Best Local Similarity 29.1%; Pred. No. 9.9e-27;			
Matches 130; Conservative 82; Mismatches 170; Indels 64; Gaps 14;			
Qy	1	MSVPDSKFGIHVYSEIGLETVLHVEPGREIDYTPARLDLFLPSAILESHDARKEHQS	60
Db	1	MSSKSSTQHTFGVHSEVQQLRWVWCAPGRAHQRLTPSNCDAFLFDVLWVDNARRDHPD	60
Qy	61	FKVIMKDRGINNVVELTDLVAETYDLASKAAKEEFIEFLEETVP-----VLTEANKKAV	114
Db	61	FMTKWRDRGVVEVWHNLLAQI--VAIPEARKWILD---NQVVPNQVGLLELDE-----I	110
Qy	115	RAFLLSKPTHEHVEFMMSGITKYL-----GVESENELIVDPMENLYFT	158
Db	111	RSYLEGLPDRLAETLIGGLSTHEFPETHGGEMLELRDAAGVA---EYLLPPLPNTLYT	167
Qy	159	RDPPASVGVGVTIHFMRVIVRRRETFLARFVRNHPKLV--KTPWYDPAWK--MPIEG	213
Db	168	RDTTCWIVGGVTNPLNYPARHEETILATAIYKHPDFGVKNVWVGFTTDMGLATLEG	227
Qy	214	GDVFIYNNETLVVGVSERTDLDTITLLAKNIKANKEVEFKRIVAINVPRKWTNLMHLDTWL	273
Db	228	GDVMEIGKGNVLIGNSERTSRQAIQLAATLFEKGAQ--RVIVAAMPKRAAMHLDTVF	285
Qy	274	TMLDKN-KFLYSPVANDVFKWDYDLVNGGAPQQLNGLPLDKLLASIN-----K	324
Db	286	TFADRDCVLIVPDIVNEIEAF-----SYRFGKPGSLELHKDRGSFVETVRDALGLK	337
Qy	325	EPVLIPICGAGATEMEIARETNFD-GTNVLAIKPGLVIGYDRNEKTNAAKAGITVLPP	383
Db	338	ENRVVETGG-----NAYVRERTQWDSGANLVCLSPGVVLAYDRNTYNTLLRKAGVEVITI	393
Qy	384	HGNQLSLGNGNARCMSPLSRKDKVKW	409
Db	394	TGAELGRGGGCHWCPIIRDADVY	419

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:03 ; Search time 182 Seconds  
(without alignments)  
1150.771 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120

Sequence: 1 MSVDSKFNHIVSEIGEL.....LGMGNARCMSPLSRKDVKN 409

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2115	99.8	408	1	ARCA_MYCHO	P41141 mycoplasma
2	1763.5	83.2	409	1	ARCA_MYCAR	P23793 mycoplasma
3	1721.5	81.2	409	2	Q9RND4	Q9rnd4 mycoplasma
4	1169.5	55.2	452	2	Q8EVF6	Q8evf6 mycoplasma
5	1103	52.0	408	2	Q7NBF0	Q7nbf0 mycoplasma
6	1057	49.9	404	1	ARCA_MYCPN	P75475 mycoplasma
7	986	46.5	409	2	Q6KI67	Q6ki67 mycoplasma
8	708.5	33.4	410	2	Q6HP29	Q6hp29 bacillus th
9	707.5	33.4	410	2	Q811I1	Q81i11 bacillus ce
10	705.5	33.3	410	2	Q73E87	Q73e87 bacillus ce
11	688	32.5	403	2	Q8KZ88	Q8kz88 granulicite
12	682.5	32.2	409	2	Q8GG81	Q8gg81 streptococc
13	681.5	32.1	411	2	Q6ZNR4	Q6znr4 bacillus li
14	681.5	32.1	413	1	ARCA_BACLI	Q6nrl3 bacillus li
15	681.5	32.1	413	2	Q6SD88	Q6sd88 bacillus li
16	679	32.0	410	1	ARCA_STRPY	P16962 streptococc
17	678.5	32.0	410	2	Q8DWQ2	Q8dwq2 streptococc
18	678.5	32.0	410	2	Q8E2K0	Q8e2k0 streptococc
19	677	31.9	410	1	ARCA_STRP3	Q8k5f0 streptococc
20	672	31.7	411	2	Q6TK74	Q6tk74 streptococc
21	670.5	31.6	408	2	Q93K67	Q93k67 enterococcu
22	660	31.1	413	1	ARCA_CLOPE	Q46254 clostridium
23	655.5	30.9	409	2	Q9KJG1	Q9kjl1 streptococc
24	651.5	30.7	409	1	ARCA_STRPN	Q97na4 streptococc
25	650	30.7	410	2	Q8GND5	Q8gnd5 streptococc
26	648.5	30.6	411	2	Q6GDG7	Q6gdg7 staphylococ
27	644.5	30.4	411	1	ARCA_STAAW	Q8nuk7 staphylococ
28	644.5	30.4	411	2	Q7AS72	Q7as72 staphylococ
29	644.5	30.4	411	2	Q6G639	Q6g639 staphylococ
30	641.5	30.3	411	1	ARCL_STAEP	Q8cgg5 staphylococ
31	640.5	30.2	411	1	ARCA_STAAW	P63553 staphylococ

32	640.5	30.2	411	1	ARCA_STAAW	P63554 staphylococ
33	638.5	30.1	410	1	ARCA_LACLC	Q9k576 lactococcus
34	638.5	30.1	410	2	Q9KGV5	Q9kqv5 lactococcus
35	638	30.1	408	1	ARCA_LISIN	Q92fr7 listeria in
36	632	29.8	410	1	ARCA_LISMO	Q8vas0 listeria mo
37	631.5	29.8	410	1	ARCA_LACLA	P58013 lactococcus
38	631	29.8	410	2	Q725C1	Q725c1 listeria mo
39	625	29.5	409	1	ARCA_LACSK	O53088 lactobacill
40	624.5	29.5	410	2	Q73QJ2	Q73qj2 treponema d
41	624.5	29.5	468	2	Q8RDD8	Q8rdd8 thermoanaer
42	621.5	29.3	409	2	Q65ZT1	Q65zt1 borrelia ga
43	617.5	29.1	415	2	Q8VM56	Q8vm56 enococcus
44	613	28.9	411	1	ARCL_STAEP	Q8cmw1 staphylococ
45	612.5	28.9	410	1	ARCA_BORBU	O51781 borrelia bu

ALIGNMENTS

RESULT 1

ID	ARCA_MYCHO	STANDARD;	PRT;	408 AA.
AC	P41141;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).			
GN	Name=arca;			
OS	Mycoplasma hominis.			
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.			
OX	NCBI_taxid=2098;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92396053; PubMed=1522817;			
RA	Harasawa R., Koehimizu K., Kitagawa M., Asada K., Kato I.;			
RT	"Nucleotide sequence of the arginine deiminase gene of Mycoplasma hominis.";			
RL	Microbiol. Immunol. 36:661-665(1992).			
CC	-!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).			
CC	-!- PATHWAY: Arginine degradation via arginine deiminase; first step.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).			
CC	-!- SIMILARITY: Belongs to the arginine deiminase family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; D13314; BAA02571.1; -.			
DR	HAWAP; MF_00242; -; 1.			
DR	InterPro; IPR003198; Amidino trans.			
DR	InterPro; IPR003876; Arg_deimnase.			
DR	Pfam; PF02274; Amidinotransf; 1.			
DR	PRINTS; PR01466; ARGDEIMINASE.			
DR	TIGRFAMs; TIGR01078; arca; 1.			
KW	Arginine metabolism; Hydrolase.			
FT	INSTR MET 0 0 By similarity.			
FT	ACT_SITE 396 396 Amidino-cysteine intermediate (By similarity).			
SQ	SEQUENCE 408 AA; 46182 MW; 53A1D6373DBBE93 CRC64;			

Query Match 99.8%; Score 2115; DB 1; Length 408;

Best Local Similarity 100.0%; Pred. No. 7e-137;

Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SVFDSKFNHIVSEIGELTVLHVEPGREIDYITPARLDELLSFALSHDARKEHQS 61

Db 1 SVFDSKFNHIVSEIGELTVLHVEPGREIDYITPARLDELLSFALSHDARKEHQS 60

Qy 62 VKMKDGRINVELTDLVAETDYLASKAAKBEFTFLEETVFLTEANKKAVRAFLSK 121

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Db 122 PTHMVEFMMSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRR 181
Db 121 PTHMVEFMMSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRR 180
Qy 182 ETLFARFVRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILLA 241
Db 181 ETLFARFVRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILLA 240
Qy 242 KNIKANKVEFKRIVAINVVKWNLMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLVNG 301
Db 241 KNIKANKVEFKRIVAINVVKWNLMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLVNG 300
Qy 302 GAEPQQLNGPLDCLKLASIINKEPVLPIPGAGATEMEIARETNFDCGTNYLAIKPGLVI 361
Db 301 GAEPQQLNGPLDCLKLASIINKEPVLPIPGAGATEMEIARETNFDCGTNYLAIKPGLVI 360
Qy 362 GYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db 361 GYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 408

RESULT 2
ARCA MYCAR
ID ARCA MYCAR STANDARD; PRT; 409 AA.
AC P23793;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).
GN Name=arca;
OS Mycoplasma arginini.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2094;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ATCC 23838;
RX MEDLINE=91034196; PubMed=7765234; DOI=10.1016/0168-1656(94)90050-7;
RA Misawa S., Aoshima M., Takaku H., Matsumoto M., Hayashi H.;
RT "High-level expression of Mycoplasma arginine deiminase in Escherichia coli and its efficient renaturation as an anti-tumor enzyme.";
RL J. Biotechnol. 36:145-155(1994).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91034196; PubMed=2228248;
RA Ohno T., Ando O., Sugimura K., Taniai M., Suzuki M., Fukuda S.,
RN Nagase Y., Yamamoto K., Azuma I.;
RT "Cloning and nucleotide sequence of the gene encoding arginine deiminase of Mycoplasma arginini.";
RL Infect. Immun. 58:3788-3795(1990).
RN [3]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=KM101;
RX MEDLINE=90220524; PubMed=2325633;
RA Kondo K., Sone H., Yoshida H., Toida T., Kanatani K., Hong Y.-M.,
RN "Cloning and sequence analysis of the arginine deiminase gene from Mycoplasma arginini.";
RT Mol. Gen. Genet. 221:81-86(1990).
CC -1- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -1- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the arginine deiminase family.
CC
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CC or send an email to license@isb-sib.ch).
CC EMBL; X54141; CAA38080.1; -
CC EMBL; X54312; CAA38210.1; -
CC EMBL; X52459; CAA36693.2; -
CC PIR; A41465; A41465.
CC PDB; 1LXY; X-ray; A/B=1-409.
CC HAMAP; MF 00242; -; 1.
CC InterPro; IPR003198; Amidino trans.
CC InterPro; IPR003876; Arg deiminase.
CC Pfam; PF02274; Amidinotransf; 1.
CC TIGRFAMS; TIGR01078; arca; 1.
CC 3D-structure; Arginine metabolism; Direct protein sequencing;
KW Hydrolase.
FT INIT_MET 0 0
FT ACT_SITE 397 397 Amidino-cysteine intermediate (By
FT similarity).
FT I -> T (in Ref. 3).
FT CONFLICT 75 75
FT CONFLICT 119 119 A -> S (in Ref. 3).
FT CONFLICT 125 125 E -> K (in Ref. 2).
FT CONFLICT 374 409 EAAGIKVLPHGNQLSLGMGNARCMSPLSRKDVKW -> D
FT KQDYLRPISI (in Ref. 3).
FT SEQUENCE 409 AA; 46376 MW; 71EC4E8D7FB69D61 CRC64;

Query Match 83.2%; Score 1763.5; DB 1; Length 409;
Best Local Similarity 82.2%; Pred. No. 9.1e-113;
Matches 336; Conservative 36; Mismatches 36; Indels 1; Gaps 1;

Qy 2 SVFDSKFGNHVYSEIGELETVLVHEPGRIDYITPARLDELLFSALESHEADKHEHQS 61
Db 1 SVFDSKFGNHVYSEIGELESVLVHEPGRIDYITPARLDELLFSALESHEADKHEHQS 60
Qy 62 VKIMKRGINWVELTDLVAETDYDLASAKAEETETLEETVPLTPEANKKAVRAFLLSK 121
Db 61 VAEKANDINVELLDVAETDYDLASAKAEETLEETVPLTPEANKKAVRAFLLSK 120
Qy 122 PT-HEMVEFMMSGITKYELGVSENELIVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRR 180
Db 121 KTSRELVEIMMAGITKYDLGIEADHEHLDVDPNPNLYFTRDPFASVGVNGVTIHFMYIYVRRQ 180
Qy 181 RETLFASVFRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILL 240
Db 181 RETLFASVFRNHPKLVKTPWYDPAKMPIDGGDVFIYNNETLVGVSERTDLDITILL 240
Qy 241 AKNIKANKVEFKRIVAINVVKWNLMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLV 300
Db 241 AKNIKANKVEFKRIVAINVVKWNLMLHLDTWLMDKNKFLYSPITANDVFKFWDYDLV 300
Qy 301 GGABPQQLNGPLDCLKLASIINKEPVLPIPGAGATEMEIARETNFDCGTNYLAIKPGLV 360
Db 301 GGABPQQLNGPLDCLKLASIINKEPVLPIPGAGATEMEIARETNFDCGTNYLAIKPGLV 360
Qy 361 IGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409
Db 361 IGYDRNEKNTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW 409

RESULT 3
Q9RND4
ID Q9RND4 PRELIMINARY; PRT; 409 AA.
AC Q9RND4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Arginine deiminase.
GN Name=arca;
OS Mycoplasma arthritidis.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG6;
```

GO; GO:0016990; F:arginine deiminase activity; IEA.  
DR GO; GO:0006527; P:arginine catabolism; IEA.  
DR InterPro; IPR003198; Amidino trans.  
DR InterPro; IPR003876; Arg\_deiminase.  
DR Pfam; PF02274; Amidinotransf.; 1.  
DR PRINTS; PR01466; ARGDEIMINASE.  
DR Complete proteome.  
KW  
SQ SEQUENCE 452 AA; 51045 MW; B25CCD15165E59F4 CRC64;

Query Match 55.2%; Score 1169.5; DB 2; Length 452;  
Best Local Similarity 56.4%; Pred. No. 5, 8e-72;  
Matches 237; Conservative 68; Mismatches 92; Indels 23; Gaps 4

Qy 1 MSVPD--SKFGNIHYVSIIGLETVLVHVEPGREIDYITPARDELFLFSAILESHDKAKH 58  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 43 MSSIDKNSLNGINGVYSIGELKEVLVHTPGDEIRYTAPSRLEELLFSAVLKADTAIEEH 102  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 59 QSFVKIMKDRGINVELTDVAETVDLASKAAKESFIETFLEETPVLTTEANKKAVRAFL 118  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 103 KGFVILQNNGIKVIQLCDLVARTYELCSKEVRNFSIQYLDEALPVLKKEIRPVVKDYL 162  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 119 LSKPTHEMVEFMMSGITKYELGVSENELIVDPMPNLFTROPFAVGNGVTIHFMYIV 178  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 163 LSPTVQVMRQMGGILANELNIKODNPLIIDGMENLFTRDPFASMGNGVINCHKYPT 222  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 179 RRRETLLFARFVRNHPKLVTPTYVD-PAMKMPIEGGDVFIIYNNETLVVGVSERTDLDTI 237  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 223 RKREVIFSRFVTNNPKYKNTPRYFDIVGNNGTIEGDDIFIYNSKTLVIGNSERTNFAAI 282  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 238 TLLAKNIKANKEVEFKRIVALNPKNWIMLDLTWLMDKKKFLYSPTANDVFKWDYD 297  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 283 ESAVKIQANKDCCTFERIWINVPPMPNMLHDLTWLMDYDFLYSPNMNVKLTIWEID 342  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 298 LVNGGAEPQPOLNGLP-----LDKLASIINKPEVLPIPGAGAGATEMETARETNFD 348  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 343 -----LNKPVKFVEKKGTLEEVLSIIDKKPLIIPAGKANQLDIDIETHFD 391  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Qy 349 GTNYLAIKPLGLVIGYDRNEKTNAALKAGITVLPFHGNQLSLGMGNARCWSMPLSRKV 408  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 392 GTNYLTIAPGVVGYERNEKTKALVEAGIKVLSFNQSLSLGMGSARCWSMPLIRENLK 451  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 5

Q7NBFO PRELIMINARY; PRT; 408 AA.

ID Q7NBFO AC Q7NBFO  
IC Q7NBFO  
AD Q7NBFO  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Arca (EC 3.5.3.6).  
GN ORFNames=MGA.1220;  
OS Mycoplasma gallisepticum.  
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
NCBI\_taxid=2096;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX PADLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;  
RA Papazisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,  
RT Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;  
RT "The complete genome sequence of the avian pathogen Mycoplasma  
RL gallisepticum strain R(10w)".  
RL Microbiology 149:2307-2316(2003).  
DR EMBL; AE016968; AAP56679.1; -.  
DR HSSP; P23793; ILXY.  
DR DR GO:0016990; F:arginine deiminase activity; IEA.  
DR GO:0001677; F:hydrolase activity; IEA.  
DR GO:0006527; P:arginine catabolism; IEA.  
DR InterPro; IPR003198; Amidino trans.  
DR InterPro; IPR003876; Arg\_deiminase.  
DR Pfam; PF02274; Amidinotransf.; 1.  
DR PRINTS; PR01466; ARGDEIMINASE.  
KW Complete proteome; Hydrolase.

```
SQ SEQUENCE 408 AA; 47084 MW; 36EC0BF5A6A8F58A CRC64;
Query Match 52.0%; Score 1103; DB 2; Length 408;
Best Local Similarity 52.2%; Pred. No. 1.9e-67;
Matches 213; Conservative 79; Mismatches 102; Indels 14; Gaps 4;
QY 8 FNGIHVYSEIGLETLVHVEPGREIDYITPARLDELLFSAILESHDARKHQSFVKIMKD 67
DB 7 FNRIRVYSEIGKLRKVLVHTFGKELDYVTPQRLDELLFSSLLNPIKARQEHETFKILED 66
QY 68 RGINNVVELTDLVAETDYLASKAAKEEFITETLPVLTTEANKAVRAFLSKPTHE-- 125
DB 67 HDVECVQLSTLTAQTFQAVNSKIQEFINRWLDECLPVLSEINRLKVDYLYKSLATNPQV 126
QY 126 MYEFNMGSIGTKYELGVSENELVDPMNLYFTDRPPFASVGVNGVTIHFMRIVVRRETLF 185
DB 127 MIRKMSGILAKEVGIOSEVELADPMNLYFTDRPPFASVGVNGVTIHFMRIVVRRETLF 186
QY 186 ARFVFRNHPKLVKTWYDDYDPAMKMPLEGDDVFIYNNETLVVGVSBERTDLDITILLAKNIK 245
DB 187 ADPFISHPHEYNAPKYYSREDKYSIEGGDLFVYDDKTLVIGVSETEKKAISLAELR 246
QY 246 ANKEVEFKRIVAINVPMKWNLMHLDTWLTMLDKXKFLYSPANDVFKWDYDLVNGGARP 305
DB 247 QNDTSFEKIVAINVPMKWNLMHLDTWLTMLDYKFLYSPNMVGVLKIWEIDLIIH----- 301
QY 306 QP-----QINGLPDLKLASIINKEPVLPIPGGAGATEMEIARETNPDGTNYLAIKPGLV 360
DB 302 -PTLIWRELE-SLEGFLSMVIGKATLIPVAGEDSTQIEDVETNFATNPLVLIQPGV 359
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
DB 360 VGYDRNYKTNQALRDAGVKYVISWNGDQLSLGMSARCMSPLYRDPK 407
RESULT 6
ARCA MYCPN
ID ARCA MYCPN STANDARD; PRT; 404 AA.
AC P75475; P75474;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase)
DE (AD).
GN Name=arCA; OrderedLocusNames=MPN304; ORFNames=MP531/MP532;
OS Mycoplasma pneumoniae;
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633; DOI=10.1093/nar/24.22.4420;
RA Himmelreich R., Hilbert H., Plegens H., Firkl E., Li B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae.";
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).
CC -!- PATHWAY: Arginine degradation via arginine deiminase; first step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the arginine deiminase family.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to several
CC frameshifts that produce two separate ORFs.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
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DR EMBL; AE000052; AAB96180.1; ALT FRAME.
DR EMBL; AE000052; AAB96179.1; ALT_FRAME.
DR HAMAP; MF 00242; atypical; 1.
DR InterPro; IPR003198; Amidino.trans.
DR InterPro; IPR003876; Arg deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PRO1466; ARGDEIMINASE.
KW Arginine metabolism; Complete proteome; Hydrolase;
KW Hypothetical protein.
FT ACT_SITE 394 394 Amidino-cysteine intermediate (By
FT similarity).
SQ SEQUENCE 404 AA; 45478 MW; 22A99F5437A7E3BE CRC64;
Query Match 49.9%; Score 1057; DB 1; Length 404;
Best Local Similarity 52.0%; Pred. No. 2.6e-64;
Matches 211; Conservative 76; Mismatches 107; Indels 12; Gaps 5;
QY 7 KFGIHVYSEIGLETLVHVEPGREIDYITPARLDELLFSAILESHDARKHQSFVKIMK 66
DB 2 KYN-INVHSEIGQLQTVLHVHTPGNEIRRIISPRLLDLLFSAVIBPDTAIOEHOTFCOLLQ 60
QY 67 DRGINNVVELTDLVAETDYLASKAAKEEFITETLPVLTTEANKAVRAFL--SKPT 123
DB 61 EQNEVQLTDLTATTFDKANATAQNFITWLDQAEFKLTPEKRYAKQVLLQKAKST 120
QY 124 HEMVEFMGSGITKYELGVES--ENELIVDPMNLYFTDRPPFASVGVNGVTIHFMRIVVR 181
DB 121 LSMVRSMMGGIDKRVAAANTINGDFLVDPMNLYFTDRPPFASVGVNGVTIHFMRIVVR 180
QY 182 ETLFARFVRNHPKLVKTPWYDPAMKMPLEGDDVFIYNNETLVVGVSBERTDLDITILLA 241
DB 181 ETLFASPIFANHPITIAARKFYFKPIDMGITIEGGDFIVYDQQTVMVGLSERTEAAINLA 240
QY 242 KNIKANKEVEFKRIVAINVPMKWNLMHLDTWLTMLDKXKFLYSPANDVFKWDYDLVNG 301
DB 241 KXIQDSTSEKRLFVINVPQLPNLMHLDTWLTMLDKXKFLYSPNMLAVLKAWRIDF-- 297
QY 302 GAEPQQLNGL--PLDKLASIINKEPVLPIPGGAGATEMEIARETNPDGTNYLAIKPGL 359
DB 298 -TDPALKWNETAGDLSTLHTIIGKPMPLIPAGADANQTEIDITHFDGTNYLTIPSV 356
QY 360 VIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRK 405
DB 357 VVGARNKLTHTQLEAAAGVKVIAFKGNQLSLGMSARCMSPLVK 402
RESULT 7
QSKI67 PRELIMINARY; PRT; 409 AA.
ID Q6KI67
AC Q6KI67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=arCA; OrderedLocusNames=MWOB2230;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmatataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Stange-Thomann N., Smith C., Decaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang S., Wilkinson J., Nicol R., Nusbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017308; AAT2709.1; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino.trans.
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DR InterPro; IPR003876; Arg_deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 409 AA; 47022 MW; 8A2PDF56914614D6 CRC64;

Query Match 46.5%; Score 986; DB 2; Length 409;
Best Local Similarity 48.4%; Pred. No. 2e-59;
Matches 198; Conservative 73; Mismatches 120; Indels 18; Gaps 7;

QY 11 IHVYSEIGELETVLVHVEPGREIDYITPARLDELLEFSAILESADARKEHQSFKVIMKDRGI 70
DB 8 INVFSIEGELQVLLKRPGEVENLTPDYLOQLFDDIPYLPPIQKEHDYFAQTLNRGV 64
SQ SEQUENCE 409 AA; 47022 MW; 8A2PDF56914614D6 CRC64;

QY 71 NVVELTDLVAETDYLASKAAKEEFTELEETVPVLTEANKKAVRAFLLSKPTHEWVEPM 130
DB 65 EVLYLEKLAEEA--LVDKGLREEFVDRILKSGQADVNAH--QTLKBYLLSFSNEELIQKI 121
SQ MSGITK-----YELGVSENELIVPMPLNYETROPFPASVGVNGVTHFMRYIVR 179
DB 122 MGVKNEIETSKKTHLYEL-MEDHYFYLDPMPNLYETROPFAASVGDGLTINKKREPAR 180
QY 180 RRETLFARFVRNHPKLVK--TPWYDPAKMPLEGGDVFIYNNETLVGVVSERTDLDIT 237
DB 181 RRESLFMEYIIKYHPRFAKHNVPIWLDRDYKFPFIEGGDELINNEETIAIGVSARTSAKAI 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTWLDKKNKLYSPIANDVFKFWDYD 297
DB 241 ERLAKNL-FSQNKIKKVLAEIIPKRAFMLHDTVFTWVDYDKFTIHFAGQPKGNMNIY 299
QY 298 LVNGGAEPQ--LNGPLDKLASIIN-KEPVLIPICGAGATEMEIARETNFDCGTNYLA 354
DB 300 ILEKGADEETLKITHRTSLMEALKEVLDLSELVLIPCGGDV--IASAREQWNDGNTLA 357
QY 355 IKPGLVIGYDNEKTNAAKAGITVLPFHGNQSLGMGNARCMSMPLSRKDV 407
DB 358 IAPGVVVYDNRVYNSVTLREHGIIEVIEVLSSELSRGRGGPRCMSGMPVIRKDI 410

RESULT 9
Q81111
ID Q81111 PRELIMINARY; PRT; 410 AA.
AC Q81111;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN OrderedLocusNames=BC0406;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galloway N., Candelon B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RL Nature 423:87-91(2003).
DR EMBL; AF016999; AAP07446.1; -.
DR HSP; PI3981; IRXX.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR InterPro; IPR003876; Arg_deiminase.
DR Pfam; PF02274; Amidinotransf; 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arca; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 410 AA; 46980 MW; 3D3AE8489168BD73 CRC64;

Query Match 33.4%; Score 707.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 2.5e-40;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVYSEIGELETVLVHVEPGREIDYITPARLDELLEFSAILESADARKEHQSFKVIMKDRGI 70
DB 5 IHVTSIEGELQVLLKRPGEVENLTPDYLOQLFDDIPYLPPIQKEHDYFAQTLNRGV 64
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QY 71 NVVELTDLVAETDYLASKAAKEEFIEFTLETPVLTTEANKAVAFLLSKPTHEWVEFM 130
Db 65 EVLYLEKLAEEA--LVDDKLEEFVDRILKEGQADVAVAH--QTLLKYLSSFSNEELIQKI 121
QY 131 MSGITK-----YELGVSESENELIVDPMPNLYFTRDPFAASVGDGLTINKMREPAR 179
Db 122 MGVVRKNEIETSKKTHLYEL-MEDHYPPYLDPMNLYFTRDPFAASVGDGLTINKMREPAR 180
QY 180 RRETLFARFVRNHPKLVK--TPWYDYPAMKVPKEGGDVFIYNNETLVVGVSERTDLDTI 237
Db 181 RRESLFMEYIIKYHPRFAKHNVPWLDRDYKFPKEGGDELINELTETIAIGVSARTSAKAI 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWDY 296
Db 241 ERLAKNL-FSRQNKIKKVLAIKPCRAFPHLDTVFTMVDYDKFTIHPAIQPGKGNMNIY 299
QY 297 DLVNGGAEPQPOL-NGLPDLKLLASII-KEPVLIPIGGAGATEMEIARETNFDTGNYLA 354
Db 300 ILEKGSDEETLKITHRTSLMEALKEVLGSELVLI PCGGGDV--IASAREQWNGDSNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSMPLSRKDV 407
Db 358 IAPGVVVTYDRNVSVNTLLREHGIEVIEVLSSELSRGRGPRCMSGMPIVRKDI 410

RESULT 10
Q73E87
ID Q73E87 PRELIMINARY; PRT; 410 AA.
AC Q73E87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Arginine deiminase (EC 3.5.3.6).
GN Name=arCa;
DE Bacillus cereus (strain ATCC 10987);
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Shores K.A., Fouts D.E., Tourasse N.J., Anguoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.B., Fraser C.M., Read T.D.;
RT "the genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.",
RL Nucleic Acids Res. 32:1977-988 (2004).
DR EMBL; AE017265; AAS39407.1; -.
DR TIGR; BCE0472; -.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino.trans.
DR Pfam; PF02274; Amidinotransf. 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arCa; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 410 AA; 46938 MW; 8D7846C9D206579A CRC64;

Query Match 33.3%; Score 705.5; DB 2; Length 410;
Best Local Similarity 40.9%; Pred. No. 3.5e-40;
Matches 169; Conservative 70; Mismatches 151; Indels 23; Gaps 10;

QY 11 IHVVSIGEITVLVHPGREGIDVITPARLDLFFSAILSHDARKEHOSFVKIMKDRGI 70
Db 5 IHVTSIGEITVLLKRPKGEVENLTPDYLOQLLFDIDIPYLIQKHHYFAQTLANRGV 64
QY 71 NVVELTDLVAETDYLASKAAKEEFIEFTLETPVLTTEANKAVAFLLSKPTHEWVEFM 130
Db 65 EVLYLEKLAEEA--LVDDKLEEFVDRILKEGQADVAVAH--QTLLKYLSSFSNEELIQKI 121
QY 131 MSGITK-----YELGVSESENELIVDPMPNLYFTRDPFAASVGDGLTINKMREPAR 179
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Db 122 MGVVRKNEIETSKKTHLYEL-MEDHYPPYLDPMNLYFTRDPFAASVGDGLTINKMREPAR 180
QY 180 RRETLFARFVRNHPKLVK--TPWYDYPAMKVPKEGGDVFIYNNETLVVGVSERTDLDTI 237
Db 181 RRESLFMEYIIKYHPRFAKHNVPWLDRDYKFPKEGGDELINELTETIAIGVSARTSAKAI 240
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWDY 296
Db 241 ERLAKNL-FSRQNKIKKVLAIKPCRAFPHLDTVFTMVDYDKFTIHPAIQPGKGNMNIY 299
QY 297 DLVNGGAEPQPOL-NGLPDLKLLASII-KEPVLIPIGGAGATEMEIARETNFDTGNYLA 354
Db 300 ILEKGSDEETLKITHRTSLMEALKEVLGSELVLI PCGGGDV--IASAREQWNGDSNTLA 357
QY 355 IKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSMPLSRKDV 407
Db 358 IAPGVVVTYDRNVSVNTLLREHGIEVIEVLSSELSRGRGPRCMSGMPIVRKDI 410

RESULT 11
Q8KZ88
ID Q8KZ88 PRELIMINARY; PRT; 403 AA.
AC Q8KZ88;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Arginine dihydrolase (EC 3.5.3.6).
GN Name=arCa;
OS Granulicatella elegans.
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Granulicatella.
OX NCBI_TaxID=137732;
RN [1]
RP SEQUENCE FROM N.A.
RA Sato S., Inoue M.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB091333; BAC11861.1; -.
DR HSSP; P13981; 1RXX.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006527; P:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino.trans.
DR InterPro; IPR003876; Arg.deiminase.
DR Pfam; PF02274; Amidinotransf. 1.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRFAMs; TIGR01078; arCa; 1.
KW Hydrolase.
SQ SEQUENCE 403 AA; 45437 MW; 0BA6C55314CF7844 CRC64;

Query Match 32.5%; Score 688; DB 2; Length 403;
Best Local Similarity 38.7%; Pred. No. 5.4e-39;
Matches 159; Conservative 73; Mismatches 157; Indels 22; Gaps 8;

QY 9 NGIHVVSIGEITVLVHPGREGIDVITPARLDLFFSAILSHDARKEHOSFVKIMKDR 68
Db 3 NPIHVVSIGEITVLLKRPKGEVENLTPDYLERLLFPDDIPYLEDAQKHEDAFAETLRNA 62
QY 69 GINVVVELTDLVAETDYLASKAAKEEFIEFTLETPVLTTEANKAVAFLLSKPTHEWVE 128
Db 63 GVEVLVLEQLAAEAIDAA--GVRBEFVDEWLSE-AGVASVASQAKKHHLLSLPFDLVL 119
QY 129 FMMSGITKVELGV-----ESNELIVDPMPNLYFTRDPFAASVGVNGVTHIFMRYIVR 179
Db 120 KTMEGFRKTEVQAEATTLAGMETDYPFVVDPMNLYFTRDPFATMANGVSLNHVADTR 179
QY 180 RRETLFARFVRNHPKLVK--VKTWPYDYPAMKVPKEGGDVFIYNNETLVVGVSERTDLDTI 237
Db 180 NEETIYGVYIFTYHPVGVNGKVPFPFNRTEDTRIEGGDELVLSEKVLAVGISQRTDARS 239
QY 238 TLLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSP-IANDVFKFWDY 297
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Db 240 EKLKII---AETDFKQVLAUFVIGENRKFHMLDVTFTTHIDYDKFTTHBPEIQGLKV--FS 294
QY 298 LVNGGAEPQQLNGLPLDKLLASINKEPV-LIPICGAGATEMEIARETNFDGTNYLAIK 356
Db 295 ITKGEMVPFVIELTDEKLENVLAKALGLSVTLIPCG--GGDPVEAREQWNGDSNTLITA 352
QY 357 PCLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407
Db 353 PGEVVVYDRNVVNTBIELEKYGIKLHKGSELVGRGGPRCMSPFERENL 403

RESULT 12
Q8GG81 PRELIMINARY; PRT; 409 AA.
ID Q8GG81;
AC Q8GG81;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE AdS.
GN Name=adS;
OS Streptococcus suis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I9841/1;
RA Winterhoff N., Goethe R., Gruening P., Valentin-Weigand P.;
RT "Identification and Characterization of Two Temperature-Induced
RT Surface-associated Proteins of Streptococcus suis with High Homologies
RT to Members of the Arginine Deiminase System of Streptococcus
RT pyogenes.";
RL J. Bacteriol. 0:0-0(2002).
RL EMBL; AF546864; AAN76306.1; -.
DR HSP; P13981; 1RX.
DR GO; GO:0016990; F:arginine deiminase activity; IEA.
DR GO; GO:0006527; F:arginine catabolism; IEA.
DR InterPro; IPR003198; Amidino trans.
DR Pfam; PF02274; Arg deiminase.
DR PRINTS; PR01466; ARGDEIMINASE.
DR TIGRPFAMs; TIGR01078; arca; 1.
DR SEQUENCE 409 AA; 46345 MW; 4DCC04E37B40394C CRC64;

Query Match 32.2%; Score 682.5; DB 2; Length 409;
Best Local Similarity 39.4%; Pred. No. 1.3e-38;
Matches 164; Conservative 76; Mismatches 145; Indels 31; Gaps 12;

QY 11 IHVSEIGELETVLVHPEGREIDYITPARLDELLFSAILESHDARKEHOSFVKIMKDRGI 70
Db 6 IHVSEIGKLVKMLHRRPKETENLMPDYLERLLPDDIPFLEDAQKEHDAFAQALRDGV 65
QY 71 NVVELTDLVAETDYLASKAAKEEFTETLEETVPVLTEANKKAVRAFLLS-KPTHEMVFE 129
Db 66 EVLYLEKLAARS--LVTPEIRQFIDYLEE--ANIRGRATKAIKRLMSIEDNOELVEK 122
QY 130 MMSGTYKVELG-----VESENELIVDPMNPLYFTRDPPASVGVNGVTIHFMYI 177
Db 123 TMAGVQKAEPLKIPSEKGLDLDLVSSYPFALDPMNPLYFTRDPPATIGNAVSLNHMYSE 182
QY 178 VRRRTLFARFVRNHPKL-VKTPWYDPAKMPLEGSDVFIYNNETLVGVGSERTDLDIT 236
Db 183 TRNRETLGKVIPTHPEYGGKVPVLYNREETTRIEGGDELVLSDVLAVGISQRTDAAS 242
QY 237 ITLLAKNIKANKEVEFKRIVAINVVKWNTLMLHDLTWLMDKNKFLYSP-IANDVFKP-- 293
Db 243 IEKLVNI--FERHVGFKKVLAFAEFANNRKFHMLDVTFTWVDYDKFTIHPETEGDLRVFSV 301
QY 294 -WDYLVNGGAEPQQLNGLPLDKLLASINKEPV-LIPICGAGATEMEIARETNFDGTN 351
Db 302 TYENDTLHIEE-----HG-DLAELLAANLGLKVELIRCGGDM--VAAGREQWNGDSN 353
QY 352 YLAIKPGLVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKDV 407
```

```
Db 354 TLTTPAGVVVVYKGNITITNAILESKGLRIKIGSELVGRGGPRCMSPFEREDI 409

RESULT 13
Q62NR4 PRELIMINARY; PRT; 411 AA.
ID Q62NR4;
AC Q62NR4;
DT 25-OCT-2004 (TremBLrel. 28, Created)
DT 25-OCT-2004 (TremBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Arginine deiminase.
GN ORFNames=BU01912;
OS Bacillus licheniformis DSM 13.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=279010;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 14580;
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,
RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,
RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,
RA Berka R.M.;
RT "Complete genome sequence of the industrial bacterium Bacillus
RT licheniformis and comparisons with closely related Bacillus species.";
RL Genome Biol. 5:R77-R77(2004).
DR EMBL; CP000002; AAU25597.1; -.
DR SEQUENCE 411 AA; 47182 MW; 98BFE4887FEC2C6E CRC64;

Query Match 32.1%; Score 681.5; DB 2; Length 411;
Best Local Similarity 38.4%; Pred. No. 1.5e-38;
Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;

QY 11 IHVSEIGELETVLVHPEGREIDYITPARLDELLFSAILESHDARKEHOSFVKIMKDRGI 70
Db 5 IHVSEIGPLKTVMLKRPGRELENITPEYLERLLFDDIPFLPAVOKEHDDQFAETUKQQA 64
QY 71 NVVELTDLVAETDYLASKAAKEEFTETLEETVPVLTEANKKAVRAFLLSKPTHEMVFE 130
Db 65 EVLYLEKLTAEALDDA--LVREQFIDELLTESKADINGAYDR-LKEFLLTFDADSMVEQV 121
QY 131 MSGTYKVELGVSESNEL-----IVDPMNPLYFTRDPPASVGVNGVTIHFMYIYVR 180
Db 122 MSGIRKNELEREKSHLHELMEHYPFYLDPMNPLYFTRDPPAAATIGSLTINKKEPAR 181
QY 181 RETLFARFVRNHPKL-V-KTPWYDPAKMPLEGSDVFIYNNETLVGVGSERTDLDIT 238
Db 182 RESLFMYIINHPRFKGHEIPVMDLDRDFKNIEGGDELVLNEETVAIGVSERTTAAIE 241
QY 239 LLAKNIKANKEVEFKRIVAINVVKWNTLMLHDLTWLMDKNKFLYSP-IANDVFKWDYDL 298
Db 242 RLVRNL-PQOSRIRRVLAVEIPKSRAPMHLDTVFTWVDRDQFTIHPAQ----- 290
QY 299 VNGGAEPQQLNGLPLDKLLASINKEPVLP-----IGGAGATEMEIARE 344
Db 291 ---GPEGDMRIFVLERGKTADEIHTTEHNLPEVLKRTGLSLDVNLIFCGGDEIASARE 347
QY 345 TNFDGTNYLAIKPGVIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSR 404
Db 348 QWNGDSNTLAIPAGVVVYDRNYISNECLRQGIKVIIEIPSGELSRGRGPRCMSPLYR 407
QY 405 KDVK 408
Db 408 EDVK 411

RESULT 14
ARCA_BACLI
ID ARCA_BACLI STANDARD; PRT; 413 AA.
AC O86131;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
```

05-JUL-2004 (Rel. 44, Last annotation update)  
Arginine deiminase (EC 3.5.3.6) (ADI) (Arginine dihydrolase) (AD).

Name=arCa;  
Bacillus licheniformis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
NCBI\_TaxID=1402;

SEQUENCE FROM N.A.  
STRAIN=ATCC 14580;

MEDLINE=99069319; PubMed=9851988;  
Magnouj A, de Souza Cabral T.F., Stalon V., Vander Wauwen C.;

The arcABC gene cluster, encoding the arginine deiminase pathway of  
Bacillus licheniformis, and its activation by the arginine repressor

argR;  
J. Bacteriol. 180:6468-6475(1998).

!- CATALYTIC ACTIVITY: L-arginine + H(2)O = L-citrulline + NH(3).  
!- PATHWAY: Arginine degradation via arginine deiminase; first step.

!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
!- SIMILARITY: Belongs to the arginine deiminase family.

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the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL; Y17554; CAA76777.1; -;  
HMAP; MF 00242; -; 1.

InterPro; IPR003198; Amidino trans.  
InterPro; IPR003876; Arg.deiminase.

Pfam; PF02274; Amidinotransf.; 1.  
PRINTS; PR01466; ARGDEIMINASE.

TIGRFAMs; TIGR01078; arCa; 1.  
Arginine metabolism; Hydrolase.

ACT\_SITE 402 402  
Amidino-cysteine intermediate (By  
similarity).

SEQUENCE 413 AA; 47427 MW; 57BB97714CAA5480 CRC64;  
Query Match 32.1%; Score 681.5; DB 1; Length 413;  
Best Local Similarity 38.4%; Pred. No. 1.5e-38;

Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;  
11 IHVSEIGLETVLVHPEGRGIDYITPARLDLLESAILESADARKEHQSFVKIMKDRGI 70  
7 IHVSEIGPLKTVMLKRPGRLENLTPYLERLLFDIDPFLPAVQKEHQDFAETLKQOGA 66

71 NVVELTDLVAETVDLASKAAKEBFIFTEETVPLTEANKKAVRAFLSKPTHEMVEFM 130  
67 EVLYLEKLTAEALDDA--LVREQFIDELLTESKADINGAYDR-LKEFLLTDFDADSMVEQV 123

131 MSGITKYELGVSENEL-----IVDPMPNLYFTDRPPASVGVNGVTIHFMYRIVRR 180  
124 MSGIRKNELEEREKSHLHLMEDHYFPYLDPMNLYFTDRPAAAGSLTINKKKEPARR 183

181 RETLFARFVFNHPKLV--KTPWYDYDPAMKMPTEGGDVFIYNNETLVGVGSERTDLDIT 238  
184 RESLFMYIINHHPFKGHEIPVWLRDFFKNIEGGDELVLNEETVAIGVSERTTAQAE 243

239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKPLYSPIANDVFKFWDYDL 298  
244 RLVRNL-FQRSIRRLVLAIVEIPKSRAPMHLDTVFTWDRDQFTIHPAIO-----292

299 VNGGAEPQPOLNGLPLDKLLASIIINKEPVLIP-----IGGAGATEMEIARE 344  
293 ---GPEGDMRIFVLERGKTADIEHTTEHNLPVLRKLTGLSDVNLIFCGGGDEIASARE 349

345 TNFDGTNYLAIKPGLVIGYDRNEKTNAALKAAGITVLPFFHGNQLSLGMGNARCMSPILSR 404  
350 QWNDSNTLALAPGVVVTYDRNYISNECLREQGKIVIEIPSGELSRGRGRCMSPMLYR 409

405 KDKV 408  
410 EDVK 413

Search completed: April 6, 2005, 06:26:25  
Job time : 185 secs

Db 410 EDVK 413

RESULT 15  
Q65D88 PRELIMINARY; PRT; 413 AA.

AC Q65D88;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Arginine deiminase (EC 3.5.3.6).  
GN ORFNames=BLI04163;

Bacillus licheniformis DSM 13.  
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=279010;  
RN [1]

SEQUENCE FROM N.A.  
RP STRAIN=DSM 13;

RX PubMed=15383718;  
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,

Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,  
Ehrenreich A., Gottschalk G.;

"The Complete Genome Sequence of Bacillus licheniformis DSM13, an  
Organism with Great Industrial Potential.";

J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
RL EMBL; AE017333; AAU42976.1; -;

KW Hydrolase.  
SQ SEQUENCE 413 AA; 47427 MW; 57BB97714CAA5480 CRC64;

Query Match 32.1%; Score 681.5; DB 2; Length 413;  
Best Local Similarity 38.4%; Pred. No. 1.5e-38;

Matches 163; Conservative 66; Mismatches 152; Indels 43; Gaps 7;  
11 IHVSEIGLETVLVHPEGRGIDYITPARLDLLESAILESADARKEHQSFVKIMKDRGI 70

7 IHVSEIGPLKTVMLKRPGRLENLTPYLERLLFDIDPFLPAVQKEHQDFAETLKQOGA 66  
71 NVVELTDLVAETVDLASKAAKEBFIFTEETVPLTEANKKAVRAFLSKPTHEMVEFM 130

67 EVLYLEKLTAEALDDA--LVREQFIDELLTESKADINGAYDR-LKEFLLTDFDADSMVEQV 123  
131 MSGITKYELGVSENEL-----IVDPMPNLYFTDRPPASVGVNGVTIHFMYRIVRR 180

124 MSGIRKNELEEREKSHLHLMEDHYFPYLDPMNLYFTDRPAAAGSLTINKKKEPARR 183  
181 RETLFARFVFNHPKLV--KTPWYDYDPAMKMPTEGGDVFIYNNETLVGVGSERTDLDIT 238

184 RESLFMYIINHHPFKGHEIPVWLRDFFKNIEGGDELVLNEETVAIGVSERTTAQAE 243  
239 LLAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKPLYSPIANDVFKFWDYDL 298

244 RLVRNL-FQRSIRRLVLAIVEIPKSRAPMHLDTVFTWDRDQFTIHPAIO-----292  
299 VNGGAEPQPOLNGLPLDKLLASIIINKEPVLIP-----IGGAGATEMEIARE 344

293 ---GPEGDMRIFVLERGKTADIEHTTEHNLPVLRKLTGLSDVNLIFCGGGDEIASARE 349  
345 TNFDGTNYLAIKPGLVIGYDRNEKTNAALKAAGITVLPFFHGNQLSLGMGNARCMSPILSR 404

350 QWNDSNTLALAPGVVVTYDRNYISNECLREQGKIVIEIPSGELSRGRGRCMSPMLYR 409  
405 KDKV 408

410 EDVK 413

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:04 ; Search time 174 Seconds  
(without alignments)  
909.109 Million cell updates/sec

Title: US-10-674-666-1

Perfect score: 2120  
Sequence: 1 MSVFDKFNHGVSEIGEL.....LGMGNARCMSPLSRKDVKW 409

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_16Dec04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2120	100.0	409	5	AAE16134	AAE16134 Mycoplasma
2	2120	100.0	409	5	ABG311996	ABG311996 M. hominu
3	2120	100.0	409	8	ADP79607	ADP79607 Mycoplasma
4	2116	99.8	409	8	ADP79608	ADP79608 Mycoplasma
5	2112	99.6	409	5	AAE16136	AAE16136 Mycoplasma
6	2112	99.6	409	8	ADP79609	ADP79609 Mycoplasma
7	2110	99.5	409	5	AAE16135	AAE16135 Mycoplasma
8	2109	99.5	408	2	AAW89442	AAW89442 Mycoplasma
9	2108	99.4	409	5	AAE16137	AAE16137 Mycoplasma
10	2108	99.4	409	8	ADP79610	ADP79610 Mycoplasma
11	1807.5	85.3	410	5	ABG311995	ABG311995 M. arthri
12	1797.5	84.8	409	8	ADP79613	ADP79613 Mycoplasma
13	1796.5	84.7	409	2	AAW89441	AAW89441 Mycoplasma
14	1793.5	84.6	409	8	ADP79616	ADP79616 Mycoplasma
15	1793.5	84.6	409	8	ADP79615	ADP79615 Mycoplasma
16	1789.5	84.4	409	8	ADP79614	ADP79614 Mycoplasma
17	1764.5	83.2	410	5	ABG311994	ABG311994 M. argini
18	1764.5	83.2	410	8	ADP79611	ADP79611 Mycoplasma
19	1763.5	83.2	410	5	ABE76127	ABE76127 Mycoplasma
20	1760.5	83.0	410	8	ADP79612	ADP79612 Mycoplasma
21	1753.5	82.7	409	2	AAW89440	AAW89440 Mycoplasma
22	1733.5	81.8	409	2	AAE24528	AAE24528 Arginine
23	1732.5	81.7	410	2	AAW65454	AAW65454 Arginine
24	1632.5	77.0	405	2	AAE05713	AAE05713 Arginine
25	1081.5	51.0	264	2	AAE20500	AAE20500 Cell grow

26	1067.5	50.4	263	2	AAE10854	AAE10854 Arginine
27	707.5	33.4	410	8	ADS27663	ADS27663 Bacterial
28	682.5	32.2	432	8	ADM77935	ADM77935 S. suis A
29	681.5	32.1	413	5	ABG32003	ABG32003 B. lichen
30	681.5	32.1	413	8	ADP79625	ADP79625 Bacillus
31	679	32.0	411	1	AAE70278	AAE70278 Streptoco
32	679	32.0	411	5	ABP26975	ABP26975 Streptoco
33	679	32.0	411	5	ABG31997	ABG31997 S. pyogen
34	679	32.0	411	7	ADC56694	ADC56694 Streptoco
35	679	32.0	411	8	ADP79619	ADP79619 Streptoco
36	678.5	32.0	410	5	ABP26974	ABP26974 Streptoco
37	670.5	31.6	408	5	ABG32004	ABG32004 E. faecal
38	670.5	31.6	408	8	ADP79626	ADP79626 Enterococ
39	667.5	31.5	417	7	ADC96521	ADC96521 E. faeciu
40	655	30.9	413	5	ABG32002	ABG32002 C. perfri
41	655	30.9	413	8	ADP79624	ADP79624 Clostridi
42	652.5	30.8	409	8	ADK47759	ADK47759 Streptoco
43	652.5	30.8	413	8	ADR94569	ADR94569 Novel S.
44	651.5	30.7	409	5	ABG31998	ABG31998 S. pneumo
45	651.5	30.7	409	6	ABU02672	ABU02672 S. pneumo

ALIGNMENTS

RESULT 1  
AAE16134  
ID AAE16134 standard; protein; 409 AA.  
XX  
AC AAE16134;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis wild type arginine deiminase (ADI).  
XX  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour.  
XX  
OS Mycoplasma hominis.  
XX  
PN WO200183774-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
(PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;  
XX  
DR WPI; 2002-097497/13.  
XX  
PT Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Example 3; Fig 1; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis wild type ADI  
SQ Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;

Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELETVLVHPEGRIDYITPARLDELLFSALESHEADKHEQS 60  
DB 1 MSVFDKNGIHVYSEIGELETVLVHPEGRIDYITPARLDELLFSALESHEADKHEQS 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETPVLTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETPVLTEANKKAVRAFLLS 120

QY 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGNVGTTHFMYIIVRR 180  
DB 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGNVGTTHFMYIIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITLL 240  
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFWDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFWDYDLVN 300

QY 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVLV 360  
DB 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVLV 360

QY 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409

RESULT 2  
ID ABG31996 standard; protein; 409 AA.  
AC ABG31996;  
DT 06-AUG-2003 (revised)  
DT 15-NOV-2002 (first entry)  
DE M. hominus arginine deiminase gene, HOMADIPRO.  
KW Arginine deiminase; cytostatic; ADI; polyethylene glycol; PEG; arginine;  
KW citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer;  
KW auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.  
XX Mycoplasma hominis.  
OS WO200244360-A2.  
PN 06-JUN-2002.  
PD 19-SEP-2001; 2001WO-US029184.  
PF 28-NOV-2000; 2000US-00723546.  
PR (PHOE-) PHOENIX PHARMACOLOGICS INC.  
PA Clark MA;  
PI WPI; 2002-619003/66.  
DR Compound for treating tumor such as melanoma, hepatoma or sarcoma in a  
PT patient, comprises arginine deiminase covalently bonded by a linking  
PT group, such as succinimide to polyethylene glycol.  
XX Example 1; Fig 1; 59pp; English.  
PS The invention discloses a compound comprising arginine deiminase (ADI)  
CC covalently bonded by a linking group to polyethylene glycol (PEG) having  
CC a total weight average molecular weight of about 1000-5000. Also  
CC disclosed is a method for enhancing the circulating half life or the

tumouricidal activity of arginine deiminase by modifying the arginine  
deiminase by covalently bonding the arginine deiminase by a linking group  
to PEG. Normal cells can synthesise arginine from citrulline in a 2 step  
process catalysed by argininosuccinate synthase and argininosuccinate  
lyase. In contrast, many cancerous cells do not express argininosuccinate  
synthase and are, therefore, auxotrophic for arginine. Arginine deiminase  
catalyses the conversion of arginine to citrulline and can be used to  
eliminate arginine from the cancerous cells. The compound is useful for  
treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
for treating and inhibiting metastases in a patient. When compared to  
native arginine deiminase the compound retains most of its enzymatic  
activity, is far less antigenic, has a greatly extended circulating half-  
life, and is much more efficacious in the treatment of tumours. The  
sequence presented is the Mycoplasma hominus arginine deiminase gene,  
CC HOMADIPRO. (Updated on 06-AUG-2003 to correct OS field.)  
XX

Sequence 409 AA;

Query Match 100.0%; Score 2120; DB 5; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELETVLVHPEGRIDYITPARLDELLFSALESHEADKHEQS 60  
DB 1 MSVFDKNGIHVYSEIGELETVLVHPEGRIDYITPARLDELLFSALESHEADKHEQS 60

QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETPVLTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETPVLTEANKKAVRAFLLS 120

QY 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGNVGTTHFMYIIVRR 180  
DB 121 KPTHEWVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGNVGTTHFMYIIVRR 180

QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITLL 240  
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVVGVSERTDLDITLL 240

QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFWDYDLVN 300  
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFWDYDLVN 300

QY 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVLV 360  
DB 301 GGAEPPQNLGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGVLV 360

QY 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409  
DB 361 IGYDRNEKTNAAKAAAGITVLPFHGNQLSLGNGNARCMSPLSRKDVVKW 409

RESULT 3  
ADP79607  
ID ADP79607 standard; protein; 409 AA.

XX ADP79607;  
AC ADP79607;  
DT 04-NOV-2004 (first entry)  
DE Mycoplasma hominis arginine deaminase.  
XX Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme.  
XX Mycoplasma hominis.  
OS WO2004046309-A2.  
PN 03-JUN-2004.  
PD 29-SEP-2003; 2003WO-US030770.  
PF 18-NOV-2002; 2002US-0427497P.

XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX Clark MA;  
XX WPI; 2004-431965/40.  
DR Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
XX Claim 18; SEQ ID NO 1; 89pp; English.  
XX  
XX The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritidis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma hominis arginine deaminase.  
XX  
XX Sequence 409 AA;  
SQ  
Query Match 100.0%; Score 2120; DB 8; Length 409;  
Best Local Similarity 100.0%; Pred. No. 1.5e-193;  
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSVFSKFNHIVYSEIGELTVLHVEPGREIDYITPARLDELLFSALESHEKDARKEHQS 60  
Db 1 MSVFSKFNHIVYSEIGELTVLHVEPGREIDYITPARLDELLFSALESHEKDARKEHQS 60  
Qy 61 FVKIMKORGINNVETLDVAETDYLASKAAKEEFTETLEETVPVLTANKKAVRAFLLS 120  
Db 61 FVKIMKORGINNVETLDVAETDYLASKAAKEEFTETLEETVPVLTANKKAVRAFLLS 120  
Qy 121 KPTHEWVFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEWVFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGNVGTIHFMYIYVR 180  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDLDITILL 240  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Qy 301 GGAEPQOLNGLPLDKLLASIIINKEPVLPIPIGGAGATEWETARETNFGTNYLAIKPGIV 360  
Db 301 GGAEPQOLNGLPLDKLLASIIINKEPVLPIPIGGAGATEWETARETNFGTNYLAIKPGIV 360  
Qy 361 IGYDRNEKTNALKAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409  
Db 361 IGYDRNEKTNALKAAGITVLPFHGNQSLGNGNARCMSMPLSRKDVKW 409  
RESULT 4  
ADP79608  
ID ADP79608 standard; protein; 409 AA.  
AC ADP79608;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX Mycoplasma hominis arginine deaminase variant.  
DE

XX Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
XX Mycoplasma hominis.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 112 /label= K112E  
FT /note= "wild-type Lys is substituted with with Glu"  
FT  
XX  
XX W02004046309-A2.  
XX  
XX 03-JUN-2004.  
PD  
XX 29-SEP-2003; 2003WO-US030770.  
PF  
XX 18-NOV-2002; 2002US-0427497P.  
PR  
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.  
PA  
XX Clark MA;  
PI  
XX WPI; 2004-431965/40.  
XX  
XX Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
XX Claim 18; SEQ ID NO 2; 89pp; English.  
PS  
XX  
XX The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritidis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma hominis arginine deaminase variant.  
XX  
XX Sequence 409 AA;  
SQ  
Query Match 99.8%; Score 2116; DB 8; Length 409;  
Best Local Similarity 99.8%; Pred. No. 3.5e-193;  
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MSVFSKFNHIVYSEIGELTVLHVEPGREIDYITPARLDELLFSALESHEKDARKEHQS 60  
Db 1 MSVFSKFNHIVYSEIGELTVLHVEPGREIDYITPARLDELLFSALESHEKDARKEHQS 60  
Qy 61 FVKIMKORGINNVETLDVAETDYLASKAAKEEFTETLEETVPVLTANKKAVRAFLLS 120  
Db 61 FVKIMKORGINNVETLDVAETDYLASKAAKEEFTETLEETVPVLTANKKAVRAFLLS 120  
Qy 121 KPTHEWVFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEWVFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGNVGTIHFMYIYVR 180  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDLDITILL 240  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300



QY 301 GGAEPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVVKW 409  
Db 361 IGYDRNEKTNAAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVVKW 409  
RESULT 5  
AAE16136  
ID AAE16136 standard; protein; 409 AA.  
AC AAE16136;  
XX  
DT 26-MAR-2002 (first entry)  
XX  
DE Mycoplasma hominis modified arginine deiminase (ADI) #2.  
KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
KW septic shock; tumour; mutant; mutein.  
XX  
OS Mycoplasma hominis.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"  
FT  
FN WO200183774-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014116.  
XX  
PR 04-MAY-2000; 2000US-00564559.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Ensor CM, Holtsberg FW, Clark MA;  
XX  
DR WPI; 2002-097497/13.  
XX  
XX Modified arginine deiminase for improved manufacturing processes and for  
PT treating cancer, is mutated to be free of a pegylation site at or  
PT adjacent to its catalytic region.  
XX  
PS Disclosure; Page 31-32; 34pp; English.  
XX  
CC The invention relates to a modified arginine deiminase (ADI) for improved  
CC manufacturing processes. The process comprises ADI modified to be free of  
CC at least one pegylation site at or adjacent to its catalytic region. ADI  
CC catalyses the conversion of arginine to citrulline and may be used to  
CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
CC and inhibiting metastasis of tumour cells and other disease states. The  
CC present sequence is Mycoplasma hominis modified ADI protein  
XX  
SQ Sequence 409 AA;  
Query Match 99.6%; Score 2112; DB 5; Length 409;  
Best Local Similarity 99.8%; Pred No. 8.5e-193;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MSVFDSEKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLSAILSHDARKHQHS 60  
Db 1 MSVFDSEKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELFLSAILSHDARKHQHS 60  
QY 61 FVKIMKDRGINVVELTDLVAETDYLSKAAKEEPIETLEETVPVLTEANKKAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETDYLSKAAKEEPIETLEETVPVLTEANKKAVRAFLLS 120

QY 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVGVTIHFMYIIVRR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMPNLYFTRDPFASVGVGVTIHFMYIIVRR 180  
QY 181 RETLPAFVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSETDLDITLL 240  
Db 181 RETLPAFVFRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVGVGSETDLDITLL 240  
QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKELYSPIANDVFKFDYDLVN 300  
QY 301 GGAEPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQQLNGPLDPLKLLASIIINKEPVLPIPIGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
QY 361 IGYDRNEKTNAAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVVKW 409  
Db 361 IGYDRNEKTNAAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVVKW 409  
RESULT 6  
ADP79609  
ID ADP79609 standard; protein; 409 AA.  
XX  
AC ADP79609;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE Mycoplasma hominis arginine deiminase variant.  
KW Arginine deiminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
OS Mycoplasma hominis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 210 /label= P210S  
FT /note= "wild-type Pro is substituted with Ser"  
XX  
FN WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
PF 29-SEP-2003; 2003WO-US030770.  
XX  
PR 18-NOV-2002; 2002US-0427497P.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
DR WPI; 2004-431965/40.  
XX  
PT Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
PS Claim 18; SEQ ID NO 3; 89pp; English.  
XX  
CC The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deiminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deiminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritidis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or



CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
 CC useful for improving liver function in an individual. The present  
 CC sequence represents a Mycoplasma hominis arginine deaminase variant.

XX Sequence 409 AA;

Query Match 99.6%; Score 2112; DB 8; Length 409;  
 Best Local Similarity 99.8%; Pred. No. 8.5e-193;  
 Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLESAILESHDARKEHQ 60  
 DB 1 MSVFDKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLESAILESHDARKEHQ 60  
 QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFLETETVPVLTTEANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFLETETVPVLTTEANKKAVRAFLLS 120  
 QY 121 KPTHEWVFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIIVRR 180  
 DB 121 KPTHEWVFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIIVRR 180  
 QY 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVGVSERTDLDITILL 240  
 DB 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVGVSERTDLDITILL 240  
 QY 241 AKNIKANKEVEFKRIVAINVPKWTNMLHDLTWTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIVAINVPKWTNMLHDLTWTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 QY 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
 DB 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
 QY 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVKW 409  
 DB 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVKW 409

RESULT 7  
 AAEL16135  
 ID AAEL16135 standard; protein; 409 AA.

XX AC AAEL16135;

XX DT 26-MAR-2002 (first entry)

XX DE Mycoplasma hominis modified arginine deiminase (ADI) #1.

XX KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
 KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
 KW septic shock; tumour; mutant; mutein.

XX OS Mycoplasma hominis.  
 OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Misc-difference 111

FT /note= "Wild type Lys substituted with Pro"

FT Misc-difference 112

FT /note= "Wild type Lys substituted with Glu"

XX PN WO200183774-A2.

XX PD 08-NOV-2001.

XX PF 02-MAY-2001; 2001WO-US014116.

XX PR 04-MAY-2000; 2000US-00564559.

XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.

XX PI Ensor CM, Holtsberg FW, Clark MA;

XX DR WPI; 2002-097497/13.

XX PT Modified arginine deiminase for improved manufacturing processes and for  
 PT treating cancer, is mutated to be free of a pegylation site at or  
 PT adjacent to its catalytic region.

XX PS Disclosure; Page 30-31; 34pp; English.

XX CC The invention relates to a modified arginine deiminase (ADI) for improved  
 CC manufacturing processes. The process comprises ADI modified to be free of  
 CC at least one pegylation site at or adjacent to its catalytic region. ADI  
 CC catalyses the conversion of arginine to citrulline and may be used to  
 CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
 CC hepatomas, sarcomas, parasitic diseases, septic shock and for treating  
 CC and inhibiting metastasis of tumour cells and other disease states. The  
 CC present sequence is Mycoplasma hominis modified ADI protein

XX SQ Sequence 409 AA;

Query Match 99.5%; Score 2110; DB 5; Length 409;  
 Best Local Similarity 99.5%; Pred. No. 1.3e-192;  
 Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSVFDKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLESAILESHDARKEHQ 60  
 DB 1 MSVFDKNGIHVYSEIGELETVLVHEPGREIDYITPARLDELLESAILESHDARKEHQ 60  
 QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFLETETVPVLTTEANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFLETETVPVLTTEANKKAVRAFLLS 120  
 QY 121 KPTHEWVFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIIVRR 180  
 DB 121 KPTHEWVFMSGITYELGVSENELIVDPMNLYFTRDPPASVGVNGVTIHFMYIIVRR 180  
 QY 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVGVSERTDLDITILL 240  
 DB 181 RETLFARVFRNHPKLVKTPWYDPAKMPTEGGDVFIYNNETLVGVSERTDLDITILL 240  
 QY 241 AKNIKANKEVEFKRIVAINVPKWTNMLHDLTWTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIVAINVPKWTNMLHDLTWTMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 QY 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
 DB 301 GGAEPQPOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAIKPGVL 360  
 QY 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVKW 409  
 DB 361 IGYDRNEKTNAALKAAAGITVLPFHGNQLSLGMGNARCMSMPLSRKDVKW 409

RESULT 8  
 AAW89442

ID AAW89442 standard; protein; 408 AA.

XX AC AAW89442;

XX DT 18-MAR-1999 (first entry)

XX DE Mycoplasma hominis arginine deiminase.

XX KW Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritis;  
 KW Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;  
 KW inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.

XX OS Mycoplasma hominis.

XX PN WO9851784-A1.

XX PD 19-NOV-1998.

XX XX

PF 12-MAY-1998; 98WO-US009575.  
 XX  
 PR 12-MAY-1997; 97US-0046200P.  
 PR 13-FEB-1998; 98US-00023809.  
 XX  
 PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 PI Clark MA;  
 XX WPI; 1999-045227/04.  
 DR  
 XX New compound comprising arginine deiminase - covalently bonded via  
 PT linking group to polyethylene glycol, to enhance the half life of  
 PT arginine by this modification.  
 XX  
 PS Claim 6; Fig 1; 30pp; English.  
 XX  
 CC The present sequence represents Mycoplasma hominis arginine deiminase.  
 CC The present invention describes: (1) a compound comprising arginine  
 CC deiminase (AD) covalently bonded via linking group to polyethylene glycol  
 CC (PEG), and having a molecular weight 12-40 kDa; and (2) a composition as  
 CC above, but where the linking group is selected from a malimide group, an  
 CC amide group, an imide group, a carbamate group, an ester group, an epoxy  
 CC group, a carboxyl group, a hydroxyl group, a carboxylate, a tyrosine  
 CC group, a cytochrome group, and/or a histidine group. AD can be used in the  
 CC treatment of tumours, e.g. melanomas, hepatomas and sarcomas, and to  
 CC inhibit metastasis. The modified AD has an enhanced circulating half life  
 XX  
 SQ Sequence 408 AA;  
 Query Match 99.5%; Score 2109; DB 2; Length 408;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-192;  
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MSVFSKFNHIVYSEIGLETLVHVEPGREIDYITPARDELLESAILESHEQHS 60  
 DB 1 MSVFSKFNHIVYSEIGLETLVHVEPGREIDYITPARDELLESAILESHEQHS 60  
 QY 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTANKKAVRAFLLS 120  
 QY 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 DB 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDDVFIYNNETLVVGVSERTDITILL 240  
 DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDDVFIYNNETLVVGVSERTDITILL 240  
 QY 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 QY 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAKPGVLV 360  
 DB 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAKPGVLV 360  
 QY 361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
 DB 361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408  
 RESULT 9  
 AAEL6137  
 ID AAEL6137 standard; protein; 409 AA.  
 AC  
 XX  
 AC  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Mycoplasma hominis modified arginine deiminase (ADI) E112, S210.  
 XX

KW Arginine deiminase; ADI; cytostatic; antibacterial; immunosuppressive;  
 KW antiparasitic; cancer; melanoma; hepatoma; sarcoma; parasitic disease;  
 XX septic shock; tumour; mutant; mutein.  
 OS Mycoplasma hominis.  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 112 /note= "Wild type Lys substituted with Glu"  
 FT Misc-difference 210 /note= "Wild type Pro substituted with Ser"  
 FT  
 XX  
 FN WO200183774-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014116.  
 XX  
 PR 04-MAY-2000; 2000US-00564559.  
 XX  
 PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
 XX  
 PI Ensor CM, Holtsberg FW, Clark MA;  
 XX WPI; 2002-097497/13.  
 DR  
 XX Modified arginine deiminase for improved manufacturing processes and for  
 PT treating cancer, is mutated to be free of a pegylation site at or  
 PT adjacent to its catalytic region.  
 XX  
 PS Example 1; Fig 2; 34pp; English.  
 XX  
 CC The invention relates to a modified arginine deiminase (ADI) for improved  
 CC manufacturing processes. The process comprises ADI modified to be free of  
 CC at least one pegylation site at or adjacent to its catalytic region. ADI  
 CC catalyses the conversion of arginine to citrulline and may be used to  
 CC eliminate arginine. ADI is useful for treating cancer, melanomas,  
 CC hepatomas, sarcomas, parasitic diseases, septic shock, and for treating  
 CC and inhibiting metastasis of tumour cells and other disease states. The  
 CC present sequence is Mycoplasma hominis modified ADI protein  
 XX  
 SQ Sequence 409 AA;  
 Query Match 99.4%; Score 2108; DB 5; Length 409;  
 Best Local Similarity 99.5%; Pred. No. 2e-192;  
 Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MSVFSKFNHIVYSEIGLETLVHVEPGREIDYITPARDELLESAILESHEQHS 60  
 DB 1 MSVFSKFNHIVYSEIGLETLVHVEPGREIDYITPARDELLESAILESHEQHS 60  
 QY 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTANKKAVRAFLLS 120  
 DB 61 FVKIMKDRGINVVELTDLVAETDYDLASKAAKEEFITFLEETVPVLTANKKAVRAFLLS 120  
 QY 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 DB 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPPASVGNVTHFMRYIVRR 180  
 QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDDVFIYNNETLVVGVSERTDITILL 240  
 DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDDVFIYNNETLVVGVSERTDITILL 240  
 QY 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 DB 241 AKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLWMLDKNKFLYSPIANDVFKFWDYDLVN 300  
 QY 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAKPGVLV 360  
 DB 301 GGAEPQOLNGLPLDKLASIINKEPVLPIGGAGATEMEIARETNFDGTNYLAKPGVLV 360  
 QY 361 IGYDRNEKTNALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

Db	361	IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMSPLSRKDKVKW	409
Db	61	FKVIMKDRGINNVVELTDLVAETYDLASAKAAKEEFTEFTLEETVPVLTBANKAVRAFLLS	120
Db	61	FKVIMKDRGINNVVELTDLVAETYDLASAKAAKEEFTEFTLEETVPVLTBANKAVRAFLLS	120
Qy	121	KPTHEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPASVGVNGVTTHFMBYIVRR	180
Db	121	KPTHEMVEFMMSGITKYELGVSENELIVDMPNLYFTRDPASVGVNGVTTHFMBYIVRR	180
Qy	181	RETLFARVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLOTITLL	240
Db	181	RETLFARVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLOTITLL	240
Qy	241	AKNIIKANKEVEFKRIVAINVPKWTNLMHLDTWLTWLDKNKFLYSPIANDVFKFWDYDLVN	300
Db	241	AKNIIKANKEVEFKRIVAINVPKWTNLMHLDTWLTWLDKNKFLYSPIANDVFKFWDYDLVN	300
Qy	301	GGAEPQOLNGLPLDKLIASIIINKEPVLIPICGGAGATEMETARETNFQGTNYLAIKPGLV	360
Db	301	GGAEPQOLNGLPLDKLIASIIINKEPVLIPICGGAGATEMETARETNFQGTNYLAIKPGLV	360
Qy	361	IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMSPLSRKDKVKW	409
Db	361	IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMSPLSRKDKVKW	409
RESULT 11			
ABG31995			
ID	ABG31995	standard; protein; 410 AA.	
XX	AC	ABG31995;	
XX	DT	15-NOV-2002 (first entry)	
XX	DE	M. arthritides arginine deiminase gene, ARTADIPRO.	
XX	KW	Arginine deiminase; cytosolic; ADI; polyethylene glycol; PEG; arginine; citrulline; argininosuccinate synthase; argininosuccinate lyase; cancer; auxotrophic; tumour; melanoma; hepatoma; sarcoma; metastasis; antigenic.	
XX	OS	Mycoplasma arthritidis.	
XX	PN	WO200244360-A2.	
XX	PD	06-JUN-2002.	
XX	PF	19-SEP-2001; 2001WO-US029184.	
XX	PR	28-NOV-2000; 2000US-00723546.	
XX	PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.	
XX	PI	Clark MA;	
XX	WPI	2002-619003/66.	
XX	PT	Compound for treating tumor such as melanoma, hepatoma or sarcoma in a patient, comprises arginine deiminase covalently bonded by a linking group such as succinimide to polyethylene glycol.	
XX	PS	Example 1; Fig 1; 59pp; English.	
XX	CC	The invention discloses a compound comprising arginine deiminase (ADI) covalently bonded by a linking group to polyethylene glycol (PEG) having a total weight average molecular weight of about 1000-50000. Also disclosed is a method for enhancing the circulating half life or the tumoricidal activity of arginine deiminase by modifying the arginine deiminase by covalently bonding the arginine deiminase by a linking group to PEG. Normal cells can synthesize arginine from citrulline in a 2 step process catalysed by argininosuccinate synthase and argininosuccinate lyase. In contrast, many cancerous cells do not express argininosuccinate synthase and are, therefore, auxotrophic for arginine. Arginine deiminase catalyses the conversion of arginine to citrulline and can be used to eliminate arginine from the cancerous cells. The compound is useful for	

Db	361	IGYDRNEKTNAAALKAAGITVLPFHGNQLSLGNGNARCMSPLSRKDKVKW	409
RESULT 10			
ADP79610			
ID	ADP79610	standard; protein; 409 AA.	
XX	AC	ADP79610;	
XX	DT	04-NOV-2004 (first entry)	
XX	DE	Mycoplasma hominis arginine deaminase variant.	
XX	KW	Arginine deaminase; cytosolic; virucide; viral replication; nitric oxide synthesis; tumour; liver function; enzyme; variant.	
XX	OS	Mycoplasma hominis.	
XX	FH	Key	
FT	Misc-difference 112	Location/Qualifiers	
FT	/label= K112E		
FT	/note= "wild-type Lys is substituted with with Glu"		
FT	/label= P210S		
FT	/note= "wild-type Pro is substituted with with Ser"		
PN	WO2004046309-A2.		
XX	PD	03-JUN-2004.	
XX	PF	29-SEP-2003; 2003WO-US030770.	
XX	PR	18-NOV-2002; 2002US-0427497P.	
XX	PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.	
XX	PI	Clark MA;	
XX	WPI	2004-431965/40.	
XX	PT	Inhibiting replication of viruses in individual, involves administering composition comprising arginine deiminase bonded to polyethylene glycol, to individual.	
XX	PS	Claim 18; SEQ ID NO 4; 89pp; English.	
XX	CC	The invention relates to inhibiting the replication of one or more viruses in an individual and involves administering to the individual a composition comprising an arginine deiminase bonded to polyethylene glycol. The method is useful for inhibiting replication of one or more viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual, where the arginine deiminase is derived from Mycoplasma e.g. M. arginini, M. hominis, M. arthritidis and its combination. It is useful for treating an individual who is suspected of having been exposed to one or more viruses, for modulating nitric oxide levels in an individual, or for selectively inhibiting viral replication in an individual. The method is also useful for treating a tumour and inhibiting replication of one or more viruses in an individual. The tumour is melanoma, sarcoma, or hepatoma. The tumour is hepatocellular carcinoma. The method is also useful for improving liver function in an individual. The present sequence represents a Mycoplasma hominis arginine deaminase variant.	
XX	Seq	Sequence 409 AA;	
Query Match			
Best Local Similarity	99.4%;	Score 2108; DB 8; Length 409;	
Matches 407; Conservative	99.5%;	Pred. No. 2e-192;	
	1; Mismatches	1; Indels	0; Gaps
Qy	1	MSVFSKNGIHVYSEIGELETVLVHEPGREIDYITPARDELLESFALESHDARKEHQS	60
Db	1	MSVFSKNGIHVYSEIGELETVLVHEPGREIDYITPARDELLESFALESHDARKEHQS	60

CC treating a tumour such as melanoma, hepatoma or sarcoma in a patient, or  
CC for treating and inhibiting metacases in a patient. When compared to  
CC native arginine deiminase the compound retains most of its enzymatic  
CC activity, is far less antigenic, has a greatly extended circulating half-  
CC life, and is much more efficacious in the treatment of tumours. The  
CC sequence presented is the Mycoplasma arthritides arginine deiminase gene,  
CC ARTADIPRO  
XX  
SQ Sequence 410 AA;

Query Match	85.3%;	Score	1807.5;	DB	5;	Length	410;	
Best Local Similarity	84.4%;	Pred.	No. 1.le-163;					
Matches	346;	Conservative	29;	Mismatches	34;	Indels	1; Gaps	1;
Qy	1	MSVDSKFNKGHVHVSSEIGELETVLVHEPGREIDYITPARLDLLELSAILESHDARKEQS	60					
Dd	1	MSVDSKFNGHVHVSSEIGELSVLVHEPGREIDYITPARLDLLELSAILESHDARKEQS	60					
Qy	61	FVKIMKORGINNVETLDLVAETYDLASAKAAKEFTIETLETVPLVTANKKAVRAFLLS	120					
Dd	61	FVALIKANDINNVETIDLVAETYDLASQAKDRLEEFEDESPVLSEAHHKVWVNFLKA	120					
Qy	121	KPT-HEMVEFMWSGTTKYVELGESNELIVDPMPNLXYTRDFSFASVGNGVTTHFWRYIVR	179					
Dd	121	KKTSRKVLMLMAGTIIKDYDLGVAEADHELIVDPMPNLXYTRDFSFASVGNGVTTHFWRYKVR	180					
Qy	180	RRETLFARFVRFRNHPKL VKTPWYDYPAMKMPIEGGDVFYNNETLIVVGSERTDLTDTTL	239					
Dd	181	RRETLSRFVFRNHPKL VNTPWYDYPAMKLSIEGGDVFIYNNDTLVVGSERTDLTDTVL	240					
Qy	240	LAKNIKANKEVEFKRIIVAINVPKWNLNHLDTWLTMLDKNKEYLSPIANDVEKFDWDYDIAV	299					
Dd	241	LAKNLVANKECEPKRIVAINVPKWNLNHLDTWLTMLDKNKEYLSPIANDVEKFDWDYDIAV	300					
Qy	300	NGGAEPOLINGLPDLKKLASTINKPEPVIIPIGGAGATEMETARETNFDGTNYLAIKPOL	359					
Dd	301	NGGAEPQPVENGLPLEKLLQSIINKPVLIPIAGECASQOMEIERETHFDGTNYAIAPGV	360					
Qy	360	VIGYDRNEKTNAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVKW	409					
Dd	361	VIGYSRNEKTNAALKAAIGIKVLFPFHGNQLSLGMGNARCMSPLSRKDVKW	410					

RESULT 12	
ADP79613	
ID	ADP79613 standard; protein; 409 AA.
XX	
AC	ADP79613;
XX	
DT	04-NOV-2004 (first entry)
XX	
DE	Mycoplasma arthritidis arginine deaminase.
XX	
KW	Arginine deaminase; cytostatic; virucide; viral replication;
XX	nitric oxide synthesis; tumour; liver function; enzyme.
XX	
OS	Mycoplasma arthritidis.
XX	
PN	WO2004046309-A2.
XX	
PD	03-JUN-2004.
XX	
PF	29-SEP-2003; 2003WO-US030770.
XX	
PR	18-NOV-2002; 2002US-0427497P.
XX	
PA	(PHOE-) PHOENIX PHARMACOLOGICS INC.
XX	
PI	Clark MA;
XX	
DR	WPI; 2004-431965/40.
XX	
PT	Inhibiting replication of viruses in individual. involves administering

composition comprising arginine deiminase bonded to polyethylene glycol, to individual.

Claim 18; SEQ ID NO 7; 89pp; English.

The invention relates to inhibiting the replication of one or more viruses in an individual and involves administering to the individual a composition comprising an arginine deaminase bonded to polyethylene glycol. The method is useful for inhibiting replication of one or more viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual, where the arginine deaminase is derived from Mycoplasma e.g. M. arginini, M. hominis, M. arthritis and its combination. It is useful for treating an individual who is suspected of having been exposed to one or more viruses, for modulating nitric oxide levels in an individual, or for selectively inhibiting viral replication in an individual. The method is also useful for treating a tumour and inhibiting replication of one ore more viruses in an individual. The tumour is melanoma, sarcoma, or hepatoma. The tumour is hepatocellular carcinoma. The method is also useful for improving liver function in an individual. The present sequence represents a Mycoplasma arthritis arginine deaminase.

Sequence 409 AA:

Query Match	84.8%	Score 1797.5	DB 8	Length 409
Best Local Similarity	84.4%	Pred. No. 1e-162		
Matches 345	Conservative 29	Mismatches 34	Indels 1	Gaps 1
QY	1	MSVDSKFNHGVHYSEIGELSETVLVHPSPGRIDVITPARLDELLSAILESHDARKEQS	60	
DB	1	MSVDSKFKGHVHYSEIGELSELVLPHPGREGIDVITPARLDELLSAILESHDARKEQSQ	60	
QY	61	FVKIMKDRGINVVELTDLVLAETVYDLASAKAAKEFIETFTVPTVLRANKKAVRAFLLS	120	
DB	61	FVAILKANDINVVEITDLVAETVYDLASQEAQDRLTIEELEDSEPLVSEAHKKVVRNFLKA	120	
QY	121	KPT-HEMVPEWMSGITTKVELGSESENELIVDPMNLYETRDPFASVGVNGVTTHFWRYIVR	179	
DB	121	KKTSRKVLVLMAGITKYDLGVEADHELIVDPMNLYETRDPFASVGVNGVTTHFWRYIVR	180	
QY	180	RRETFLFARFVRNHPKLVKTPWYYDPAKMPIEGGDVFYINNETLVVGVSRETDLDTITL	239	
DB	181	RRETFLFSRFVRNHPKLVNTPWYYDPAKLSIEGGDVFYINNDTLVVGVSRTDLDTVTL	240	
QY	240	LAKNIKANKEVEFKRIIVAINVPKTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLV	299	
DB	241	LAKNLVANKECEFKRIIVAINVPKTNLMHLDTWLTMLDKNKFYSPIANDVFKFWDYDLV	300	
QY	300	NGGAEPQPLNGLPLDKLLASINKPEPLVPIIGAGATAMEIARTFNFDGNTYLAIKPGL	359	
DB	301	NGGAEPQPVNGLPLEKLLQSIIINKPVLIPIAGEGASQMEIERETHFDGNTYLAIRPGV	360	
QY	360	VIGYDRNEKNTAAAKAGITVLPFHGNOLSLGMGNARCWSMPLSRKDYK	408	
DB	361	VIGYSRNEKNTAAAKAGIKVLPHGNOLSLGMGNARCWSMPLSRKDYK	409	

RESULT 13	
AAW89441	
ID	AAW89441 standard; protein; 409 AA.
XX	
XX	
AC	
XX	AAW89441;
DT	18-MAR-1999 (first entry)
XX	
XX	Mycoplasma arthritis arginine deiminase.
DE	
XX	
XX	Arginine deiminase; Mycoplasma arginini; Mycoplasma arthritis;
KW	Mycoplasma hominis; modified; polyethylene glycol; cancer; metastasis;
KW	inhibition; melanoma; hepatoma; sarcoma; enhanced circulating half life.
XX	
OS	Mycoplasma arthritis.
XX	
PN	W09851784-A1.

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XX 19-NOV-1998.
XX 12-MAY-1998; 98WO-US009575.
XX 12-MAY-1997; 97US-0046200P.
XX 13-FEB-1998; 98US-00023809.
XX (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX Clark MA;
XX WPI; 1999-045227/04.
XX New compound comprising arginine deiminase - covalently bonded via
XX linking group to polyethylene glycol, to enhance the half life of
XX arginine by this modification.
XX Claim 6; Fig 1; 30pp; English.
XX The present sequence represents Mycoplasma arthritis arginine
XX deiminase. The present invention describes: (1) a compound comprising
XX arginine deiminase (AD) covalently bonded via linking group to
XX polyethylene glycol (PEG), and having a molecular weight 12-40 kDa; and
XX (2) a composition as above, but where the linking group is selected from
XX a malimide group, an amide group, an imide group, a carbamate group, an
XX ester group, an epoxy group, a carboxyl group, a hydroxyl group, a
XX carbohydrate, a tyrosine group, a cysteine group and/or a histidine
XX group. AD can be used in the treatment of tumours, e.g. melanomas,
XX hepatomas and sarcomas, and to inhibit metastasis. The modified AD has an
XX enhanced circulating half life
XX Sequence 409 AA;
XX
Query Match 84.7%; Score 1796.5; DB 2; Length 409;
Best Local Similarity 84.4%; Pred. No. 1.3e-162; Indels 1; Gaps 1;
Matches 345; Conservative 29; Mismatches 34;
QY 1 MSVFDKFGHIVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQ 60
DB 1 MSVFDKFGHIVYSEIGELESVLVHEPGREIDYITPARLDELFSAILSHDARKEQ 60
QY 61 FVKIMKORGINNVETLDLVAETDYDLASKAAKEEFTEETVPTLVANKAVRAFLLS 120
DB 61 FVAILKANDINNVETLDLVAETDYDLASQEAQDRLEEFLEDEPVLSEAHKVVNF 120
QY 121 KPT-HEMVDFWMSGITKYELGVSENELIVDPMNLYETRDPPFASVGVNGVTIHF 179
DB 121 KKTSRKLVLMWAGITKYDLGVADHELIYDPMNLYETRDPPFASVGVNGVTIHF 180
QY 180 RRETLFARFVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDIT 239
DB 181 RRETLFARFVFRNHPKLVNTWYDPAKMLSTEGDVFYNNETLVVGVSERTDIT 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWNTLMHDLTWLTMLDKNKFYSPIANDFK 299
DB 241 LAKNLVANKECEFKRIVAINVPKWNTLMHDLTWLTMLDKNKFYSPIANDFK 300
QY 300 NGGAEPQOLNGLPLDKLLASINKEPVLPIPGGAGATEMETARETNDGTNYLA 359
DB 301 NGGAEPQVENGLEPLDKLLQSIINKPVLPIPAGEGASQMEIERETFDGTNY 360
QY 360 VIGYDRNKTNAALKAAGITVLPFHGNOLSLGMGNARCMSPLSRDKVK 408
DB 361 VIGYSRNETNAALKAAGIKVLPPFHGNQLSLGMGNARCMSPLSRDKVK 409

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RESULT 14

ADP79616

ID ADP79616 standard; protein; 409 AA.

XX

AC ADP79616;

XX

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DT 04-NOV-2004 (first entry)
XX Mycoplasma arthritis arginine deiminase variant.
XX Arginine deiminase; cytostatic; virucide; viral replication;
XX nitric oxide synthesis; tumour; liver function; enzyme; variant.
XX OS Mycoplasma arthritis.
XX FH Key Location/Qualifiers
XX FT Misc-difference 112
XX FT /label= K112E
XX FT /note= "wild-type Lys is substituted with with Glu"
XX PN WO2004046309-A2.
XX PD 03-JUN-2004.
XX PF 29-SEP-2003; 2003WO-US030770.
XX PR 18-NOV-2002; 2002US-0427497P.
XX PA (PHOE-) PHOENIX PHARMACOLOGICS INC.
XX PI Clark MA;
XX WPI; 2004-431965/40.
XX Inhibiting replication of viruses in individual, involves administering
XX composition comprising arginine deiminase bonded to polyethylene glycol,
XX to individual.
XX Claim 18; SEQ ID NO 10; 89pp; English.
XX The invention relates to inhibiting the replication of one or more
XX viruses in an individual and involves administering to the individual a
XX composition comprising an arginine deiminase bonded to polyethylene
XX glycol. The method is useful for inhibiting replication of one or more
XX viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,
XX where the arginine deiminase is derived from Mycoplasma e.g. M. arginini,
XX M. hominis, M. arthritis and its combination. It is useful for treating
XX an individual who is suspected of having been exposed to one or more
XX viruses, for modulating nitric oxide levels in an individual, or for
XX selectively inhibiting viral replication in an individual. The method is
XX also useful for treating a tumour and inhibiting replication of one ore
XX more viruses in an individual. The tumour is melanoma, sarcoma, or
XX hepatoma. The tumour is hepatocellular carcinoma. The method is also
XX useful for improving liver function in an individual. The present
XX sequence represents a Mycoplasma arthritis arginine deiminase variant.
XX Sequence 409 AA;
XX
Query Match 84.6%; Score 1793.5; DB 8; Length 409;
Best Local Similarity 84.1%; Pred. No. 2.4e-162; Indels 1; Gaps 1;
Matches 344; Conservative 30; Mismatches 34;
QY 1 MSVFDKFGHIVYSEIGELETVLVHEPGREIDYITPARLDELFSAILSHDARKEHQ 60
DB 1 MSVFDKFGHIVYSEIGELESVLVHEPGREIDYITPARLDELFSAILSHDARKEQ 60
QY 61 FVKIMKORGINNVETLDLVAETDYDLASKAAKEEFTEETVPTLVANKAVRAFLLS 120
DB 61 FVAILKANDINNVETLDLVAETDYDLASQEAQDRLEEFLEDEPVLSEAHKVVNF 120
QY 121 KPT-HEMVDFWMSGITKYELGVSENELIVDPMNLYETRDPPFASVGVNGVTIHF 179
DB 121 KKTSRKLVLMWAGITKYDLGVADHELIYDPMNLYETRDPPFASVGVNGVTIHF 180
QY 180 RRETLFARFVFRNHPKLVKTPWYDPAKMPTEGGDVFYNNETLVVGVSERTDIT 239
DB 181 RRETLFARFVFRNHPKLVNTWYDPAKMLSTEGDVFYNNETLVVGVSERTDIT 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWNTLMHDLTWLTMLDKNKFYSPIANDFK 299

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Db 241 LAKNLVANKCEFEKRIIVAINVPKWTNLMHLDIWTMLDKNFKLYSPIANDVFEWDYDLV 300  
QY 300 NGGAEPQQLNGLPDLKLLASIIINKEPVLPIGGAGATEMEIARETNFDGNTNLAIRPGL 359  
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGNTNLAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQSLGGMGNARCMSPLSRDKVK 408  
Db 361 VIGYSRNEKTNAAALKAAGIKVLPFHGNQSLGGMGNARCMSPLSRDKVK 409

RESULT 15  
ADP79615  
ID ADP79615 standard; protein; 409 AA.  
XX  
AC ADP79615;  
DT 04-NOV-2004 (first entry)  
XX  
DE Mycoplasma arthritis arginine deaminase variant.  
KW Arginine deaminase; cytostatic; virucide; viral replication;  
KW nitric oxide synthesis; tumour; liver function; enzyme; variant.  
XX  
OS Mycoplasma arthritis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 111  
FT /label= K111E  
FT /note= "wild-type Lys is substituted with with Glu"  
XX  
PN WO2004046309-A2.  
XX  
PD 03-JUN-2004.  
XX  
PF 29-SEP-2003; 2003WO-US030770.  
XX  
PR 18-NOV-2002; 2002US-0427497P.  
XX  
PA (PHOE-) PHOENIX PHARMACOLOGICS INC.  
XX  
PI Clark MA;  
XX  
XX WPI; 2004-431965/40.  
XX  
DR Inhibiting replication of viruses in individual, involves administering  
PT composition comprising arginine deiminase bonded to polyethylene glycol,  
PT to individual.  
XX  
PS Claim 18; SEQ ID NO 9; 89pp; English.  
XX

CC The invention relates to inhibiting the replication of one or more  
CC viruses in an individual and involves administering to the individual a  
CC composition comprising an arginine deaminase bonded to polyethylene  
CC glycol. The method is useful for inhibiting replication of one or more  
CC viruses e.g. hepatitis virus (hepatitis C virus-1b), in an individual,  
CC where the arginine deaminase is derived from Mycoplasma e.g. M. arginini,  
CC M. hominis, M. arthritis and its combination. It is useful for treating  
CC an individual who is suspected of having been exposed to one or more  
CC viruses, for modulating nitric oxide levels in an individual, or for  
CC selectively inhibiting viral replication in an individual. The method is  
CC also useful for treating a tumour and inhibiting replication of one ore  
CC more viruses in an individual. The tumour is melanoma, sarcoma, or  
CC hepatoma. The tumour is hepatocellular carcinoma. The method is also  
CC useful for improving liver function in an individual. The present  
CC sequence represents a Mycoplasma arthritis arginine deaminase variant.  
XX  
SQ Sequence 409 AA;

Query Match 84.6%; Score 1793.5; DB 8; Length 409;  
Best Local Similarity 84.1%; Pred. No. 2.4e-162;  
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKFNHIVYSEIGELETVLVHEPGRREIDYITPARDELIFSAILSHDARKEHQ 60  
Db 1 MSVFDSEKFIHIVYSEIGELSVLVHEPGRREIDYITPARDELIFSAILSHDARKEQSQ 60  
QY 61 FVKIMKDRGINNVVELTDLVAETDYDLASKAAKBEPIETFTLEETVPLTEANKKAVRAFLLS 120  
Db 61 FVALIKANDINNVETIDLVAETDYDLASQEAQRDLIEBFELEDSEPVLSAHEKVVVRNFLKA 120  
QY 121 KPT-HEMVFEFMMSGITKYVELGVSENELIVDPMENLYFTRDPPFASVGVGVTIHFMRIVR 179  
Db 121 KKTSRKLVELMMAGITKYDLGVEADHELI VDPMPNLYFTRDPPFASVGVGVTIHFMRIVR 180  
QY 180 RRETLEFARFVRNHPKLVKTPWYYDPAMKMPIEGGDVFIYNNETLVVGVSERTDLDITTL 239  
Db 181 RRETLEFARFVRNHPKLVKTPWYYDPAMKLSIEGDDVFIYNNETLVVGVSERTDLDITTL 240  
QY 240 LAKNLIKANKVEFEKRIIVAINVPKWTNLMHLDIWTMLDKNFKLYSPIANDVFEWDYDLV 299  
Db 241 LAKNLVANKCEFEKRIIVAINVPKWTNLMHLDIWTMLDKNFKLYSPIANDVFEWDYDLV 300  
QY 300 NGGAEPQQLNGLPDLKLLASIIINKEPVLPIGGAGATEMEIARETNFDGNTNLAIRPGL 359  
Db 301 NGGAEPQPVENGPLEKLLQSIINKKPVLIPIAGEGASQMEIERETHFDGNTNLAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQSLGGMGNARCMSPLSRDKVK 408  
Db 361 VIGYSRNEKTNAAALKAAGIKVLPFHGNQSLGGMGNARCMSPLSRDKVK 409

Search completed: April 6, 2005, 06:30:19  
Job time : 177 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 05:55:04 ; Search time 24 Seconds  
(without alignments)  
1272.144 Million cell updates/sec

Title: US-10-674-666-1  
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Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2120	100.0	409	3	US-09-023-809B-3
2	2120	100.0	409	4	US-09-564-559B-1
3	2120	100.0	409	4	US-09-723-546-3
4	2116	99.8	409	4	US-09-564-559B-2
5	2112	99.6	409	4	US-09-564-559B-3
6	2108	99.4	409	4	US-09-564-559B-4
7	2098.5	98.0	410	1	US-08-792-283A-8
8	2098.5	99.0	410	2	US-09-105-908-8
9	2098.5	99.0	410	3	US-09-271-713-8
10	1807.5	85.3	410	3	US-09-023-809B-2
11	1807.5	85.3	410	4	US-09-723-546-2
12	1793.5	84.6	409	4	US-09-564-559B-7
13	1789.5	84.4	409	4	US-09-564-559B-9
14	1789.5	84.4	409	4	US-09-564-559B-10
15	1785.5	84.2	409	4	US-09-564-559B-8
16	1765.5	83.3	410	1	US-08-792-283A-7
17	1765.5	83.3	410	2	US-09-105-908-7
18	1765.5	83.3	410	3	US-09-271-713-7
19	1764.5	83.2	410	3	US-09-023-809B-1
20	1764.5	83.2	410	4	US-09-723-546-1
21	1746.5	82.4	409	4	US-09-564-559B-5
22	1742.5	82.2	409	4	US-09-564-559B-6
23	1732.5	81.7	410	1	US-08-792-283A-2
24	1732.5	81.7	410	2	US-09-105-908-2
25	1732.5	81.7	410	3	US-09-271-713-2
26	1713.5	80.8	410	1	US-08-792-283A-9
27	1713.5	80.8	410	2	US-09-105-908-9

28	1713.5	80.8	410	3	US-09-271-713-9
29	1698.5	80.1	399	6	5474928-2
30	1698.5	80.1	399	6	5474928-2
31	681.5	32.1	413	4	US-09-723-546-12
32	679	32.0	411	4	US-09-723-546-6
33	670.5	31.6	408	4	US-09-723-546-13
34	667.5	31.5	417	4	US-09-107-532A-6148
35	655	30.9	413	4	US-09-723-546-11
36	652.5	30.8	409	4	US-09-583-110-4274
37	652.5	30.8	413	4	US-09-107-433-3204
38	651.5	30.7	409	4	US-09-723-546-7
39	640.5	30.2	411	3	US-08-964-652-2
40	640.5	30.2	422	3	US-09-134-001C-2931
41	625	29.5	409	4	US-09-723-546-14
42	618	29.2	420	3	US-09-134-001C-4427
43	612.5	28.9	410	4	US-09-723-546-8
44	604.5	28.5	394	4	US-09-710-279-58
45	600.5	28.3	409	4	US-09-723-546-9

ALIGNMENTS

RESULT 1  
US-09-023-809B-3  
; Sequence 3, Application US/09023809B  
; Patent No. 6183738  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PHOE0028  
; CURRENT APPLICATION NUMBER: US/09/023,809B  
; PRIOR FILING DATE: 2000-02-13  
; PRIOR APPLICATION NUMBER: 60/046,200  
; PRIOR FILING DATE: 1997-05-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-023-809B-3

Query Match	100.0.0%;	Score	2120;	DB	3;	Length	409;		
Best Local Similarity	100.0.0%;	Pred. No.	2e-212;						
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Db	1	MSVFDSEKNGIHVYSEIGEL	TVLVHVEPGREIDYITPARLDELL	FSAILESHDKARKEHQS	60				
Qy	61	FKVIMKDRGINVVELTDLVAET	YDLASAKAAKEEFIEFTLEET	PVLTEANKKAVRAFLLS	120				
Db	61	FKVIMKDRGINVVELTDLVAET	YDLASAKAAKEEFIEFTLEET	PVLTEANKKAVRAFLLS	120				
Qy	121	KPTHEWVFMSGITKYELGVSE	NELIVDPMNLYFTRDPPASVGN	GVYTIHFMYRYIVRR	180				
Db	121	KPTHEWVFMSGITKYELGVSE	NELIVDPMNLYFTRDPPASVGN	GVYTIHFMYRYIVRR	180				
Qy	181	RETLEFARVFRNHPKLVKTP	WYDPAKMPLEGDDVFIYNNET	LVGVYSERTDLOTITLL	240				
Db	181	RETLEFARVFRNHPKLVKTP	WYDPAKMPLEGDDVFIYNNET	LVGVYSERTDLOTITLL	240				
Qy	241	AKNIKANKEVEFKRIVA	INVPKNTNMLDITWLTMLDKN	KFLYSPDIANDVPKFDYDLVN	300				
Db	241	AKNIKANKEVEFKRIVA	INVPKNTNMLDITWLTMLDKN	KFLYSPDIANDVPKFDYDLVN	300				
Qy	301	CGAEPOQLNGLPDLKLLAS	IINKEPVLIPIGGAGATEMEI	ARETNFDGNTYLAIKPGLV	360				
Db	301	CGAEPOQLNGLPDLKLLAS	IINKEPVLIPIGGAGATEMEI	ARETNFDGNTYLAIKPGLV	360				
Qy	361	IGYDRNEKNTNAAKAGITV	LPFHGNQLSLGNGNARCMSP	LSRKDVKW 409					



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Db 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409

RESULT 2
US-09-564-559B-1
; Sequence 1, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-1

Query Match 100.0%; Score 2120; DB 4; Length 409;
Best Local Similarity 100.0%; Pred. No. 2e-212;
Matches 409; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
DB 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFLLS 120
DB 61 FVKIMKDRGINNVVELTDLVAETYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFLLS 120
QY 121 KPTHEMVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGNVGTIHFMYIIVRR 180
DB 121 KPTHEMVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGNVGTIHFMYIIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDGVFIYNNETLVVGVSERTDLDITILL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDGVFIYNNETLVVGVSERTDLDITILL 240
QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTKMKNKFLYSPINDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTKMKNKFLYSPINDVFKFWDYDLVN 300
QY 301 GGAEPQPOLNGLPLDKLLASIIKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPQPOLNGLPLDKLLASIIKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409
DB 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409

RESULT 4
US-09-564-559B-2
; Sequence 2, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma hominis
US-09-564-559B-2

Query Match 99.8%; Score 2116; DB 4; Length 409;
Best Local Similarity 99.8%; Pred. No. 5.3e-212;
Matches 408; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSVFDKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQS 60
QY 61 FVKIMKDRGINNVVELTDLVAETYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFLLS 120
DB 61 FVKIMKDRGINNVVELTDLVAETYDLASKAAKEEFTFLEETVPVLTEANKKAVRAFLLS 120
QY 121 KPTHEMVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGNVGTIHFMYIIVRR 180
DB 121 KPTHEMVEFMMSGITKVELGVSENELIVDPMPNLYFTTRDPFASVGNVGTIHFMYIIVRR 180
QY 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDGVFIYNNETLVVGVSERTDLDITILL 240
DB 181 RETLFARFVRNHPKLVKTPWYDPAKMPLEGDGVFIYNNETLVVGVSERTDLDITILL 240
QY 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTKMKNKFLYSPINDVFKFWDYDLVN 300
DB 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTKMKNKFLYSPINDVFKFWDYDLVN 300
QY 301 GGAEPQPOLNGLPLDKLLASIIKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
DB 301 GGAEPQPOLNGLPLDKLLASIIKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360
QY 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409
DB 361 IGYDRNEKTNAAKAGITVLPFHGNQSLGNGNARCMSPLSRKDVKW 409

RESULT 3
US-09-723-546-3
; Sequence 3, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
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Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGNVGTIHFMYIYVR 180  
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Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVKW 409  
RESULT 5  
US-09-564-559B-3  
; Sequence 3, Application US/09564559B  
; Patent No. 6635462  
; GENERAL INFORMATION:  
; APPLICANT: Ensor, Charles Mark  
; APPLICANT: Holtsberg, Frederick Wayne  
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase  
; FILE REFERENCE: PHOE0033  
; CURRENT APPLICATION NUMBER: US/09/564,559B  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 09/564,559  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: PCT/US01/14116  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 3  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-564-559B-3  
Query Match 99.6%; Score 2112; DB 4; Length 409;  
Best Local Similarity 99.8%; Pred. No. 1.4e-211;  
Matches 408; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSVFSKFNHIVYSEIGELETVLVHEPGRETDYITPARLDELLFSAILESHDARKEHQS 60  
Db 1 MSVFSKFNHIVYSEIGELETVLVHEPGRETDYITPARLDELLFSAILESHDARKEHQS 60  
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGNVGTIHFMYIYVR 180  
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Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
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Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Qy 361 IGYDRNEKTNAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVKW 409  
Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVKW 409  
RESULT 6  
US-09-564-559B-4  
; Sequence 4, Application US/09564559B  
; Patent No. 6635462  
; GENERAL INFORMATION:  
; APPLICANT: Ensor, Charles Mark  
; APPLICANT: Holtsberg, Frederick Wayne  
; APPLICANT: Clark, Mike A.  
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase  
; FILE REFERENCE: PHOE0033  
; CURRENT APPLICATION NUMBER: US/09/564,559B  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: 09/564,559  
; PRIOR FILING DATE: 2000-05-04  
; PRIOR APPLICATION NUMBER: PCT/US01/14116  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 4  
; LENGTH: 409  
; TYPE: PRT  
; ORGANISM: Mycoplasma hominis  
US-09-564-559B-4  
Query Match 99.4%; Score 2108; DB 4; Length 409;  
Best Local Similarity 99.5%; Pred. No. 3.6e-211;  
Matches 407; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 MSVFSKFNHIVYSEIGELETVLVHEPGRETDYITPARLDELLFSAILESHDARKEHQS 60  
Qy 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120  
Db 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFTEETLEETVPVLTTEANKKAVRAFLLS 120  
Qy 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGNVGTIHFMYIYVR 180  
Db 121 KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGNVGTIHFMYIYVR 180  
Qy 181 RETLFARVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Db 181 RETLFARVFRNHPKLVKTPWYDPAKMPIEGGDVFIYNNETLVVGVSERTDLDITILL 240  
Qy 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Db 241 AKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLMDKNKFLYSPDIANDVFKFWDYDLVN 300  
Qy 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Db 301 GGAEPQPOLNGLPLDKLLASIIINKEPVLPIPGGAGATEMEIARETNFDGTNYLAIKPGLV 360  
Qy 361 IGYDRNEKTNAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVKW 409  
Db 361 IGYDRNEKTNAALKAAGITVLPFFHGNQSLGNGNARCMSMPLSRKDVKW 409  
RESULT 7  
US-08-792-283A-8  
; Sequence 8, Application US/08792283A  
; Patent No. 5804183  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David  
; APPLICANT: Wang, Maoliang  
; TITLE OF INVENTION: Arginine Deiminase Derived From

;; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/792,283A  
;; FILING DATE: 31-JAN-1997  
;; CLASSIFICATION: 428  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
;; US-08-792-283A-8

Query Match 99.0%; Score 2098.5; DB 1; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
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DB |||||  
QY 1 MSVFDKFGNGIHVYSEIGLETLVHVEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFITETLEETVPLTEANKKAVRAFLLS 120  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFITETLEETVPLTEANKKAVRAFLLS 120  
DB |||||  
QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIYR 179  
DB |||||  
QY 121 QKPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIYR 180  
DB |||||  
QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSRDLDITL 239  
DB |||||  
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSRDLDITL 240  
DB |||||  
QY 240 LAKNIKANKEVEFKRIVAINVPAKWTNLMHLDITLMTLDKKNFLYSPINDVFKFWDYDLV 299  
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QY 241 LAKNIKANKEVEFKRIVAINVPAKWTNLMHLDITLMTLDKKNFLYSPINDVFKFWDYDLV 300  
DB |||||  
QY 300 NGGAEPQQLNGLPLDKLLASINKEPVLIPGGAGATEMEIARETNPDGNTYLAIRKPL 359  
DB |||||  
QY 301 NGGAEPQQLNGLPLDKLLASINKEPVLIPGGAGATEMEIARETNPDGNTYLAIRKPL 360  
DB |||||  
QY 360 VIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKQVKW 409  
DB |||||  
QY 361 VIGYDRNEKTNAAKAGITVLPFHGNQLSLGMGNARCMSPLSRKQVKW 410  
DB |||||

RESULT 8

US-09-105-908-8  
;; Sequence 8, Application US/09105908  
;; Patent No. 5916793  
;; GENERAL INFORMATION:..  
;; APPLICANT: Filpula, David  
;; APPLICANT: Wang, Maoliang  
;; TITLE OF INVENTION: Arginine Deiminase Derived From  
;; MYCOPLASMA AND POLYMER CONJUGATES CONTAINING THE SAME  
;; NUMBER OF SEQUENCES: 9  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: ROBERTS & MERCANTI  
;; STREET: 81 Tamarack Circle  
;; CITY: Skillman  
;; STATE: New Jersey  
;; COUNTRY: United States  
;; ZIP: 08558  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/105,908  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA: US/08/792,283  
;; FILING DATE: 31-JAN-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mercanti, Michael N.  
;; REGISTRATION NUMBER: 33966  
;; REFERENCE/DOCKET NUMBER: 2131055  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 609-921-3500  
;; TELEFAX: 609-921-9535  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 410 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: No. 5916793 Relevant  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Mycoplasma hominis  
;; STRAIN: PG21  
;; CELL TYPE: unicellular  
;; US-09-105-908-8

Query Match 99.0%; Score 2098.5; DB 2; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
  
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DB |||||  
QY 1 MSVFDKFGNGIHVYSEIGLETLVHVEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFITETLEETVPLTEANKKAVRAFLLS 120  
DB |||||  
QY 61 FVKIMKDRGINVVELTDLVAETDYLASKAAKEEFITETLEETVPLTEANKKAVRAFLLS 120  
DB |||||  
QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIYR 179  
DB |||||  
QY 121 QKPTHEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTIHFMYIYR 180  
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QY 180 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSRDLDITL 239  
DB |||||  
QY 181 RRETLFARFVRNHPKLVKTPWYDPAKMPLEGGDVFIYNNETLVVGVSRDLDITL 240  
DB |||||  
QY 240 LAKNIKANKEVEFKRIVAINVPAKWTNLMHLDITLMTLDKKNFLYSPINDVFKFWDYDLV 299  
DB |||||  
QY 241 LAKNIKANKEVEFKRIVAINVPAKWTNLMHLDITLMTLDKKNFLYSPINDVFKFWDYDLV 300  
DB |||||

QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIKPGL 359  
DB 301 NGGAEPQPVNLGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIKPGL 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 409  
DB 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 410

RESULT 9  
US-09-271-713-8  
; Sequence 8, Application US/09271713  
; Patent No. 6132713  
; GENERAL INFORMATION:  
; APPLICANT: Filpula, David  
; APPLICANT: Wang, Maoliang  
; TITLE OF INVENTION: Arginine Deiminase Derived From  
; TITLE OF INVENTION: Mycoplasma and Polymer Conjugates Containing the Same  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROBERTS & MERCANTI  
; STREET: 81 Tamarack Circle  
; CITY: Skillman  
; STATE: New Jersey  
; COUNTRY: United States  
; ZIP: 08558

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/271,713  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/792,283  
; FILING DATE: 31-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mercanti, Michael N.  
; REGISTRATION NUMBER: 33966  
; REFERENCE/DOCKET NUMBER: 2131055  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-921-3500  
; TELEFAX: 609-921-9535  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 410 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: No. 6132713 Relevant  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Mycoplasma hominis  
; STRAIN: PG21  
; CELL TYPE: unicellular  
US-09-271-713-8

Query Match 99.0%; Score 2098.5; DB 3; Length 410;  
Best Local Similarity 99.3%; Pred. No. 3.6e-210;  
Matches 407; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFTLEETVPVLTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFTLEETVPVLTEANKKAVRAFLLS 120  
QY 121 -KPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 179

DB 121 QKPTHEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLLFARFVRNHPKLVKTPWYDPPAMKMPIEGGDVFIYNNETLVVGVSERTDITL 239  
DB 181 RRETLLFARFVRNHPKLVKTPWYDPPAMKMPIEGGDVFIYNNETLVVGVSERTDITL 240  
QY 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDEVKFWDYDLV 299  
DB 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDEVKFWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIKPGL 359  
DB 301 NGGAEPQPVNLGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIKPGL 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 409  
DB 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 410

RESULT 10  
US-09-023-809B-2  
; Sequence 2, Application US/09023809B  
; Patent No. 6183738  
; GENERAL INFORMATION:  
; APPLICANT: Clark, Mike A  
; TITLE OF INVENTION: Modified Arginine Deiminase  
; FILE REFERENCE: PHOE0028  
; CURRENT APPLICATION NUMBER: US/09/023,809B  
; CURRENT FILING DATE: 2000-02-13  
; PRIOR APPLICATION NUMBER: 60/046,200  
; PRIOR FILING DATE: 1997-05-12  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 410  
; TYPE: PRT  
; ORGANISM: Mycoplasma arthritidis  
US-09-023-809B-2

Query Match 85.3%; Score 1807.5; DB 3; Length 410;  
Best Local Similarity 84.4%; Pred. No. 8.6e-180;  
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;  
QY 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
DB 1 MSVDSKFNHIVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60  
QY 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFTLEETVPVLTEANKKAVRAFLLS 120  
DB 61 FVKIMKDRGINVVELTDLVAETYDLASKAAKEEFTLEETVPVLTEANKKAVRAFLLS 120  
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 179  
DB 121 KTSRKLVELMAGITKYDLGVADHLLIVDPMNLYFTRDPFASVGVNGVTIHFMYIVR 180  
QY 180 RRETLLFARFVRNHPKLVKTPWYDPPAMKMPIEGGDVFIYNNETLVVGVSERTDITL 239  
DB 181 RRETLLFARFVRNHPKLVKTPWYDPPAMKMPIEGGDVFIYNNETLVVGVSERTDITL 240  
QY 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDEVKFWDYDLV 299  
DB 241 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDITLMDKNKFLYSPIANDEVKFWDYDLV 300  
QY 300 NGGAEPQOLNGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIKPGL 359  
DB 301 NGGAEPQPVNLGLPLDKLLASIIINKEPVLIPGGAGATEMEIARETNFDGTYNLAIRPGV 360  
QY 360 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 409  
DB 361 VIGYDRNEKTNAAALKAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVWK 410

RESULT 11

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US-09-723-546-2
; Sequence 2, Application US/09723546
; Patent No. 6737259
; GENERAL INFORMATION:
; APPLICANT: Clark, Mike A
; TITLE OF INVENTION: Modified Arginine Deiminase
; FILE REFERENCE: PHOE0059
; CURRENT APPLICATION NUMBER: US/09/723,546
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/023,809
; PRIOR FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-723-546-2

Query Match      85.3%; Score 1807.5; DB 4; Length 410;
Best Local Similarity 84.4%; Pred. No. 8.6e-180;
Matches 346; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHIVYSEIGELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 60
Dy 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELLFSAILESHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Dy 61 FVAILKANDINNVETIDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFMMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
Dy 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 180
Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDITTL 239
Dy 181 RRETLPFRFVRNHPKLVNTPWYDPAKMLSIGGDVFIYNNETLVVGVSERTDLDITTL 240
Qy 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKLPSPIANDVFKFWDYDLV 299
Dy 241 LAKNLVANKECEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKLPSPIANDVFKFWDYDLV 300
Qy 300 NGGAEPQPLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTYLAIRPGL 359
Dy 301 NGGAEPQPVENGLPLEKLQSLIINKKPVLIPIAGGASQMEIERETHFDGNTYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 409
Dy 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 12
US-09-564-559B-7
; Sequence 7, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 7
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-7

Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHIVYSEIGELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 60
Dy 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELLFSAILESHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Dy 61 FVAILKANDINNVETIDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFMMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
Dy 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
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; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-7

Query Match      84.6%; Score 1793.5; DB 4; Length 409;
Best Local Similarity 84.4%; Pred. No. 2.5e-178;
Matches 345; Conservative 29; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHIVYSEIGELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 60
Dy 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELLFSAILESHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Dy 61 FVAILKANDINNVETIDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFMMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
Dy 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 180
Qy 180 RRETLPARFVRNHPKLVKTPWYDPAKMPPIEGGDVFIYNNETLVVGVSERTDLDITTL 239
Dy 181 RRETLPFRFVRNHPKLVNTPWYDPAKMLSIGGDVFIYNNETLVVGVSERTDLDITTL 240
Qy 240 LAKNIKANKEVEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKLPSPIANDVFKFWDYDLV 299
Dy 241 LAKNLVANKECEFKRIIVAINVPKWTNLMHLDTWLTMLDKNKLPSPIANDVFKFWDYDLV 300
Qy 300 NGGAEPQPLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGNTYLAIRPGL 359
Dy 301 NGGAEPQPVENGLPLEKLQSLIINKKPVLIPIAGGASQMEIERETHFDGNTYLAIRPGV 360
Qy 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Dy 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 13
US-09-564-559B-9
; Sequence 9, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; CURRENT FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 09/564,559
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: PCT/US01/14116
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 9
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-9

Query Match      84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

Qy 1 MSVDSKFNHIVYSEIGELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 60
Dy 1 MSVDSKFKGIHVYSEIGELSVLVHPEGRIDYITPARLDELLFSAILESHDARKEQSQ 60
Qy 61 FVKIMKDRGINNVVELTDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Dy 61 FVAILKANDINNVETIDLVAETYLDAKAAKEEFIEFTFLEETVPVLTANKKAVRAFLLS 120
Qy 121 KPT-HEMVFMMSGITKYELGVSENELIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
Dy 121 KKTSRKLVELMMAGITKYDLGVADHLLIVDPMNLYFTTRDPFASVGNVGTIHFMRVYIVR 179
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Db 121 KTSRKLVELMMWAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDYPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSFVRNHPKLVNTPWYDYPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAPQPVENGLPLEKLLQSIINKKPVLIPIAGSAGSQMEIERETHFDGTYNIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 14
US-09-564-559B-10
; Sequence 10, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-10

Query Match 84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKFGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
Db 1 MSVFDSEKFGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
QY 61 FVKIMKDRGINVELTDLVAETDYDLASAKAEETFEETVLPVLTEANKAVRAPLIS 120
Db 61 FVAILKANDINVTETDLVAETDYDLASQAEAKDRKIEEFLEDEPVLSEAHKEVVRNFLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 179
Db 121 KTSRKLVELMMWAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDYPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSFVRNHPKLVNTPWYDYPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAPQPVENGLPLEKLLQSIINKKPVLIPIAGSAGSQMEIERETHFDGTYNIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

Search completed: April 6, 2005, 06:27:18
Job time : 26 secs
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Db 121 KTSRKLVELMMWAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 180
QY 180 RRETILFARFVRNHPKLVKTPWYDYPAMKMPTEGGDVFIYNNETLVVGVSERTDLDITL 239
Db 181 RRETILFSFVRNHPKLVNTPWYDYPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAPQPVENGLPLEKLLQSIINKKPVLIPIAGSAGSQMEIERETHFDGTYNIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
Db 361 VIGYSRNEKTNAAKAAAGIKVLPFHGNQLSLGMGNARCMSPLSRKDVK 409

RESULT 14
US-09-564-559B-10
; Sequence 10, Application US/09564559B
; Patent No. 6635462
; GENERAL INFORMATION:
; APPLICANT: Ensor, Charles Mark
; APPLICANT: Holtsberg, Frederick Wayne
; APPLICANT: Clark, Mike A.
; TITLE OF INVENTION: No. 6635462el Mutated Form Of Arginine Deiminase
; FILE REFERENCE: PHOE0033
; CURRENT APPLICATION NUMBER: US/09/564,559B
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2000-05-04
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 409
; TYPE: PRT
; ORGANISM: Mycoplasma arthritidis
US-09-564-559B-10

Query Match 84.4%; Score 1789.5; DB 4; Length 409;
Best Local Similarity 84.1%; Pred. No. 6.5e-178;
Matches 344; Conservative 30; Mismatches 34; Indels 1; Gaps 1;

QY 1 MSVFDSEKFGIHVYSEIGELETVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
Db 1 MSVFDSEKFGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILESHDARKEHQ 60
QY 61 FVKIMKDRGINVELTDLVAETDYDLASAKAEETFEETVLPVLTEANKAVRAPLIS 120
Db 61 FVAILKANDINVTETDLVAETDYDLASQAEAKDRKIEEFLEDEPVLSEAHKEVVRNFLKA 120
QY 121 KPT-HEMVEFMMSGITKYELGVSENELIVDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 179
Db 121 KTSRKLVELMMWAGITKYDLGVEADHELIYDPMPLNYFTRDPFASVGVNGVTTHFMYKVR 180
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Db 181 RRETILFSFVRNHPKLVNTPWYDYPAMKLSIEGGDVFIYNNETLVVGVSERTDLDITL 240
QY 240 LAKNIKANKEVEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 299
Db 241 LAKNLVANKECEFKRIVAINVPKWTNLMHLDTWLTMLDKNKFLYSPIANDEVKFWDYDLV 300
QY 300 NGGAPQPOLNGLPLDKLLASIIINKEPVLIPIGGAGATEMEIARETNFDGTYNLAIKPGL 359
Db 301 NGGAPQPVENGLPLEKLLQSIINKKPVLIPIAGSAGSQMEIERETHFDGTYNIAIRPGV 360
QY 360 VIGYDRNEKTNAAKAAAGITVLPFHGNQLSLGMGNARCMSPLSRKDVK 408
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